

SEQUENCE LISTING

<110> Diversa Corporation

Kerovuo, Janne

Solbak, Arne

Gray, Kevin

McCann, Ryan

Purohit, Shalaka

Gerendash, Joel

Janssen, Giselle

Dahod, Samun

<120> PECTATE LYASES, NUCLEIC ACIDS ENCODING
THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462009640

<140> To Be Assigned

<141> Concurrently herewith

<150> 60/460,842

<151> 2003-04-04

<150> 60/484,798

<151> 2003-07-03

<160> 134

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1917

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 1

gtgtctctt tagaaaaact	cgcaactgctg	gttctgtcg	gtctactgct	ttctgtcgga	60
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acaattcaac	aagcggtgga	ccaggttccc	aaagacaata	cacacccgg	180
atcaaaccgg	gtgtgtatca	gaaacagggt	cgtgtcgccg	ccggcaaacg	240
tttcgcggcg	acgatgcgag	caagaccgtc	atcacatc	tttatact	300
ggaaatacc	ggctggcatt	caccac	ttaaatgcag	acgactt	360
ctgacgttt	aaaactcctt	ccgcacccgg	tcacaagcgg	ttgcgttgc	420
gaccgcgcga	cgtttggaaa	ctgcccgtt	ctcggttggc	aggacactt	480
ggcagccgccc	acttctcaa	agactgtac	gtcgaaggcc	acgtcgattt	540
acggcctccg	ccgtgttga	gaactgcacc	attcacagca	aaggcgaagg	600
gcacactatc	gcaccagcga	ttagatggat	accggtttgc	tcttcatcg	660
acccggacgag	acacgggccc	cgagatttat	ctcggaaaggc	tttggcgaacc	720
gtcgtcttta	tcgattgctg	gctggacgca	cacatcagac	ttacgcgcgc	780
agagatctg	aacgagagaa	gaccgcgtgg	tttgccgagt	tttgcgttgc	840
gctaattcccg	tagctcg	cgcggttcc	aggcagttga	tttgcgttgc	900
ttttcgcggg	aacgctttt	cagccgcgt	gttcgcgggc	tctctgggca	960
gcagtcggaa	cgatcgctg	ggacgatgcg	cagaaaaaac	cgaacgagtg	1020
gccgaggcgt	tgcgcattgc	cgacaacgtt	gtatgcgagc	tttgcgttgc	1080
cccaagaaca	tcgacatggg	gaagccgctc	gacgaaaagg	tttgcgttgc	1140

gtgcgttaaga	agaacgattc	cacgatcgac	aatggcgca	cttacacgca	actctcggtt	1200
ctggcgccgg	tttacacggc	gcaaaaagcg	gagcggcatc	gcgagtcgtt	tctgaaggga	1260
ctcgattacc	tgttgaaggc	gcagtatcca	aacggaggct	ggccgcagg	ctatccaaac	1320
ctcaacggct	attacaaca	catcacttcc	aacgacaacg	ccatgatcg	cgtgatgaaa	1380
ctgctgcgcg	acgttagcgc	agcgaaaccg	gcgtatgcgt	tcgtcgacga	agcacgacgg	1440
acgagtgcgg	cgaaggcgg	cgaaaaagg	atcgagtgc	tactgaagac	gcaggtgg	1500
gtgaatggcc	ggcgacccgt	gtgggtgtgc	caacatgacg	aagtacacgt	cgcgcctg	1560
ccggcgagga	cgttgaatt	agtttcgct	agtgggtgt	aaagcgttga	gatcg	1620
tttttgcgt	cgatcaagaa	cccgtcgccc	gcccgtgtcg	aggcgatcga	gtcggcg	1680
gcgtgggtcg	agcaatcg	atgaaagat	ccgcggca	aacctgcgt	ggcgcgat	1740
tatgagatcg	gcaactatcg	tccgatctc	gcccgggt	acggcgt	taatgtat	1800
gtgaaacaga	tcgatgagga	acgacgaaag	aattacgc	gttacgttga	cgacgcagcg	1860
aaactactga	aaaccgacta	tcctgagtgg	aaagaaaaga	acgc	aaaga	1917

<210> 2

<211> 638

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(21)

<221> DOMAIN

<222> (28)...(308)

<223> Pectin methyl esterase domain

<221> DOMAIN

<222> (309)...(638)

<223> Catalytic domain

<400> 2

Met	Ser	Leu	Phe	Arg	Lys	Leu	Ala	Leu	Leu	Val	Leu	Cys	Gly	Leu	Leu
1															15
Leu	Ser	Val	Gly	Ala	Glu	Thr	Arg	Ala	Ser	Lys	Arg	Ile	Val	Val	Ala
															30
Ala	Asp	Gly	Ser	Gly	Asp	Val	Arg	Thr	Ile	Gln	Gln	Ala	Val	Asp	Gln
															45
Val	Pro	Lys	Asp	Asn	Thr	His	Pro	Val	Leu	Ile	Gln	Ile	Lys	Pro	Gly
															60
Val	Tyr	Gln	Glu	Gln	Val	Arg	Val	Ala	Ala	Gly	Lys	Arg	Phe	Ile	Thr
															80
Phe	Arg	Gly	Asp	Asp	Ala	Ser	Lys	Thr	Val	Ile	Thr	Tyr	Arg	Leu	Ser
															95
Ala	Leu	Gln	Ala	Gly	Asn	Thr	Arg	Leu	Ala	Phe	Thr	Thr	Phe	Val	Asn
															110
Ala	Asp	Asp	Phe	Arg	Ala	Glu	Asn	Leu	Thr	Phe	Glu	Asn	Ser	Phe	Gly
															125
Thr	Gly	Ser	Gln	Ala	Val	Ala	Leu	Phe	Val	Asp	Ala	Asp	Arg	Ala	Thr
															140
Phe	Glu	Asn	Cys	Arg	Phe	Leu	Gly	Trp	Gln	Asp	Thr	Leu	Phe	Val	Asn
															160
Gly	Ser	Arg	His	Phe	Phe	Lys	Asp	Cys	Tyr	Val	Glu	Gly	His	Val	Asp
															175
Phe	Ile	Phe	Gly	Thr	Ala	Ser	Ala	Val	Phe	Glu	Asn	Cys	Thr	Ile	His
															190
Ser	Lys	Gly	Glu	Gly	Tyr	Val	Thr	Ala	His	Tyr	Arg	Thr	Ser	Asp	Glu

195	200	205
Met Asp Thr Gly Phe Val Phe His Arg Cys Arg Leu Thr Gly Arg Asp		
210	215	220
Thr Gly Arg Gly Val Tyr Leu Gly Arg Pro Trp Arg Pro Tyr Ala Arg		
225	230	235
Val Val Phe Ile Asp Cys Trp Leu Asp Ala His Ile Arg Pro Glu Gly		
245	250	255
Trp Asp Asn Trp Arg Asp Pro Glu Arg Glu Lys Thr Ala Trp Phe Ala		
260	265	270
Glu Tyr Lys Ser Lys Gly Pro Gly Ala Asn Pro Val Ala Arg Val Ala		
275	280	285
Trp Ser Arg Gln Leu Thr Thr Glu Gln Ala Ala Glu Phe Ser Arg Glu		
290	295	300
Arg Phe Phe Ser Arg Ala Val Arg Gly Leu Ser Gly Gln Ala Asn Gln		
305	310	315
Ala Val Gly Thr Ile Ala Trp Asp Asp Ala Gln Lys Lys Pro Asn Glu		
325	330	335
Trp Tyr Ala Ser Ala Glu Ala Leu Arg Ile Ala Asp Asn Val Val Leu		
340	345	350
Tyr Gln Arg Asp Ser Gly Gly Trp Pro Lys Asn Ile Asp Met Gly Lys		
355	360	365
Pro Leu Asp Glu Lys Gly Arg Ala Gly Leu Leu Arg Val Arg Lys Lys		
370	375	380
Asn Asp Ser Thr Ile Asp Asn Gly Ala Thr Tyr Thr Gln Leu Ser Phe		
385	390	395
Leu Ala Arg Val Tyr Thr Ala Gln Lys Gln Glu Arg His Arg Glu Ser		
405	410	415
Phe Leu Lys Gly Leu Asp Tyr Leu Leu Lys Ala Gln Tyr Pro Asn Gly		
420	425	430
Gly Trp Pro Gln Phe Tyr Pro Asn Leu Asn Gly Tyr Tyr Lys His Ile		
435	440	445
Thr Phe Asn Asp Asn Ala Met Ile Gly Val Met Lys Leu Leu Arg Asp		
450	455	460
Val Ala Thr Ala Lys Pro Ala Tyr Ala Phe Val Asp Glu Ala Arg Arg		
465	470	475
Thr Ser Ala Ala Lys Ala Val Glu Lys Gly Ile Glu Cys Ile Leu Lys		
485	490	495
Thr Gln Val Val Val Asn Gly Arg Arg Thr Val Trp Cys Ala Gln His		
500	505	510
Asp Glu Val Thr Leu Ala Pro Ala Pro Ala Arg Thr Phe Glu Leu Val		
515	520	525
Ser Leu Ser Gly Gly Glu Ser Val Glu Ile Val Arg Phe Leu Met Ser		
530	535	540
Ile Lys Asn Pro Ser Pro Ala Val Val Glu Ala Ile Glu Ser Ala Val		
545	550	555
Ala Trp Phe Glu Gln Ser Gln Val Lys Asp Pro Ala Gly Lys Pro Ala		
565	570	575
Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Ile Phe Ala Gly		
580	585	590
Arg Asp Gly Val Val Lys Tyr Asp Val Lys Gln Ile Asp Glu Glu Arg		
595	600	605
Arg Lys Asn Tyr Ala Trp Tyr Val Asp Asp Ala Ala Lys Leu Leu Lys		
610	615	620
Thr Asp Tyr Pro Glu Trp Lys Glu Lys Asn Ala Lys Asp Gln		
625	630	635

<210> 3
 <211> 1416
 <212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 3

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gcgcgcgtc	tgtctcggtt	tcgagcgag	gagaatccgt	ggaaacgggt	gatgccttcg	120
atcgaaac	gcatcaagcg	acctcggtt	ccgatcgca	cggttgatct	cacggagttt	180
ggagcgaaag	gtatggacg	aacagattgc	acgttggctt	tccgtcgccg	gatcgatcga	240
tgacgaaacg	ccgggtgtgg	gagagtagtt	gttccaccgg	gttcgtatct	cactggcgcc	300
attcatttga	agagcaacgt	cgaccttcat	atctcagaag	gtactacggt	caagttcagc	360
cagaacccga	aagactacct	gcccgttgtt	ttctcggtt	ggaaaggcgt	cgaggtgttc	420
aactactcgc	cttttatcta	cgccctcgaa	caaacaaca	ttgcgatcac	tggcaagggc	480
acgctcaacg	gtcaaagcga	caacgaacac	tggtgccct	gaaacggacg	tgccgcgtac	540
ggctggaaag	aaggatgag	caatcagcgt	cccgatcgaa	atgcgctgtt	tgcgatggcc	600
gaaaaagggtg	tcccgttca	ggagcgcatt	tttggtgagg	gccattactt	aaggccgcag	660
ttcattcaac	cttatacggtt	tgagaacgtg	ctgatcgaa	gtgtcactat	tcgaaactcg	720
ccgatgtggg	aaattcatcc	ggtgtctgc	cggaatgtca	tctgtccaaa	tgtgatcatc	780
aacagtcatg	gtccaaacaa	cgacgggtgt	aatctgagt	cgtgcacgga	tgtgttgatt	840
aaggattgtg	acttcgacac	tggtgacgat	tgtatcgca	tcaagtcaagg	ccgaaatgca	900
gatggcgcc	gactgaaggc	tcctactgaa	aacattatcg	tgactggttg	tgcgatgaaa	960
gatggtcacg	gccccgattac	ggtggcagc	gagattcgg	gtgggggtgcg	aaattttc	1020
gcatccaact	gccggctcga	cagtccgaac	ctggaccatg	cattgcgggt	taagaataac	1080
gctatgcgtg	gccccgtt	ggagaatctg	cacttccgaa	atatcgacgt	cgggcaagtg	1140
gcccacgcgg	tgatcacat	cgatttcaat	tatgaggaag	gcccgaagg	atcggtcacg	1200
ccagtcgttc	gtgattacac	cgtcgatggc	cttcgcagca	cgaaaagtaa	gtacgcgctc	1260
gatgtgcagg	gcttggcgcac	ggcgcgcgatc	gtgaatctgc	gtctaaccaa	ctgcacatctc	1320
gacaatgtcg	ctgaaggaaa	tgttgtgaag	aacgtaaagg	atgcaactat	cgagaatgtc	1380
aaaatcaatg	aaaaaagcgt	tgtgcagtg	ccgtag			1416

<210> 4

<211> 471

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1) ... (28)

<221> DOMAIN

<222> (81) ... (476)

<223> Catalytic domain

<400> 4

Met	Ser	Ser	Arg	Arg	Glu	Phe	Ile	Arg	Asp	Leu	Leu	Thr	Gly	Gly	Ala
1					5				10				15		
Leu	Ile	Ala	Val	Ala	Pro	Arg	Leu	Ser	Ala	Phe	Ala	Ala	Glu	Glu	Asn
							20		25				30		
Pro	Trp	Glu	Thr	Val	Met	Pro	Ser	Ile	Val	Lys	Arg	Ile	Lys	Arg	Pro
								35	40		45				
Arg	Phe	Pro	Met	Arg	Thr	Phe	Asp	Leu	Thr	Glu	Phe	Gly	Ala	Lys	Gly
								50	55		60				
Asp	Gly	Arg	Thr	Asp	Cys	Thr	Leu	Ala	Phe	Arg	Arg	Ala	Ile	Asp	Arg
								65	70		75		80		
Cys	Thr	Asn	Ala	Gly	Gly	Gly	Arg	Val	Val	Val	Pro	Pro	Gly	Ser	Tyr
								85	90				95		

Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asp Leu His Ile Ser
 100 105 110
 Glu Gly Thr Thr Val Lys Phe Ser Gln Asn Pro Lys Asp Tyr Leu Pro
 115 120 125
 Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
 130 135 140
 Phe Ile Tyr Ala Phe Glu Gln Thr Asn Ile Ala Ile Thr Gly Lys Gly
 145 150 155 160
 Thr Leu Asn Gly Gln Ser Asp Asn Glu His Trp Trp Pro Trp Asn Gly
 165 170 175
 Arg Ala Ala Tyr Gly Trp Lys Glu Gly Met Ser Asn Gln Arg Pro Asp
 180 185 190
 Arg Asn Ala Leu Phe Ala Met Ala Glu Lys Gly Val Pro Val Gln Glu
 195 200 205
 Arg Ile Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
 210 215 220
 Tyr Arg Cys Glu Asn Val Leu Ile Glu Gly Val Thr Ile Arg Asn Ser
 225 230 235 240
 Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Ile Val Gln
 245 250 255
 Asn Val Ile Ile Asn Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
 260 265 270
 Glu Ser Cys Thr Asp Val Leu Ile Lys Asp Cys Asp Phe Asp Thr Gly
 275 280 285
 Asp Asp Cys Ile Ala Ile Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
 290 295 300
 Leu Lys Ala Pro Thr Glu Asn Ile Ile Val Thr Gly Cys Arg Met Lys
 305 310 315 320
 Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val
 325 330 335
 Arg Asn Leu Phe Ala Ser Asn Cys Arg Leu Asp Ser Pro Asn Leu Asp
 340 345 350
 His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly Gly Leu Leu Glu
 355 360 365
 Asn Leu His Phe Arg Asn Ile Asp Val Gly Gln Val Ala His Ala Val
 370 375 380
 Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Phe Thr
 385 390 395 400
 Pro Val Val Arg Asp Tyr Thr Val Asp Gly Leu Arg Ser Thr Lys Ser
 405 410 415
 Lys Tyr Ala Leu Asp Val Gln Gly Leu Ala Thr Ala Pro Ile Val Asn
 420 425 430
 Leu Arg Leu Thr Asn Cys Ile Phe Asp Asn Val Ala Glu Gly Asn Val
 435 440 445
 Val Lys Asn Val Lys Asp Ala Thr Ile Glu Asn Val Lys Ile Asn Gly
 450 455 460
 Lys Ser Val Asp Ala Val Pro
 465 470

<210> 5
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 5
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attctaaagc	agccgaaact	ttgg tacgcg	gtcgacgaag	cgacgcggat	cgcaaatcag	120
gtgatcctt	atcaacgcga	caacgggtt	tggccgaaga	atatcgacat	ggccgccatg	180
ctcatgcagg	cagaacgcga	aaaacttagt	cgcgagaaga	gcgagaccga	cacgacaatc	240
gacaacggcg	cgacgacaac	ccagctcg	tatctggca	aggcatcac	ggccaagaat	300
atcgaaagcc	atcgctcg	gttttcaaa	ggcctcgatt	ttctttcgc	catcgactac	360
ggaatggcg	gcttcccga	atttttcct	ctgcgtgacg	attattcg	cgagattacg	420
ttcaacgaca	acgcgtat	aatgtgctt	cggttgc	gcgacatacg	cgatcgaaag	480
aacgattat	tgtttgcga	tgaagagcgg	cgagcgaagg	ccgagcaggc	tgttaaggcgt	540
gcgatcccgt	tgatcctcag	cacgcaggc	gtcgtcgatg	gaaagaaaac	cgtctggcgt	600
gcccagtat	atgagaagac	attgaagccg	gcccggcgc	gaaagttcga	gccggcatca	660
ttgaccgccc	gcgagagcgt	tggcatcg	cggttttga	tgctagaaaa	accaacaccc	720
gagatcatta	acgcgtatcg	atccgcac	gcttggtaca	aggcgaacaa	catctcg	780
cttaggtgg	agaggcggaa	cgcgagaaac	attgtatca	aagacaagaa	cgcggccc	840
gtctggcgc	gcttttatca	gatcgaaacg	atgaggccg	tcttcggcgg	tcgcgtatcg	900
gtcatcagat	acgatgtat	gcagatcg	tcgaaacgtc	gaaacggata	tgcatgg	960
gtatccgaac	cgaatgagtt	gttgaatgaa	gattatccg	agtggaggac	aaggagtgcg	1020
aagcgtgcc	agatcttca	acgtccgc	cttggttcga	gatttcggac	cgtgtag	1077

<210> 6

<211> 358

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(358)

<223> Catalytic domain

<400> 6

Met	Asp	Asp	Lys	Trp	Ala	Glu	Arg	Thr	Ser	Pro	Asp	Phe	Asn	Leu	Val
1					5				10					15	
Ser	Trp	Asn	Glu	Ile	Leu	Lys	Gln	Pro	Lys	Leu	Trp	Tyr	Ala	Val	Asp
					20				25					30	
Glu	Ala	Thr	Arg	Ile	Ala	Asn	Gln	Val	Ile	Leu	Tyr	Gln	Arg	Asp	Asn
					35			40				45			
Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Ala	Ala	Met	Leu	Met	Gln	Ala
					50			55			60				
Glu	Arg	Glu	Lys	Leu	Ser	Arg	Glu	Lys	Ser	Glu	Thr	Asp	Thr	Thr	Ile
					65			70		75			80		
Asp	Asn	Gly	Ala	Thr	Thr	Thr	Gln	Leu	Ala	Tyr	Leu	Ala	Lys	Val	Ile
					85			90				95			
Thr	Ala	Lys	Asn	Ile	Glu	Ser	His	Arg	Val	Ala	Phe	Phe	Lys	Gly	Leu
					100			105				110			
Asp	Phe	Leu	Phe	Ala	Met	Gln	Tyr	Gly	Asn	Gly	Gly	Phe	Pro	Gln	Phe
					115			120				125			
Phe	Pro	Leu	Arg	Asp	Asp	Tyr	Ser	Arg	Glu	Ile	Thr	Phe	Asn	Asp	Asn
					130			135			140				
Ala	Met	Ile	Asn	Val	Leu	Arg	Leu	Leu	Arg	Asp	Ile	Ala	Asp	Arg	Lys
					145			150		155				160	
Asn	Asp	Tyr	Val	Phe	Val	Asp	Glu	Glu	Arg	Arg	Ala	Lys	Ala	Glu	Gln
					165			170				175			
Ala	Val	Arg	Arg	Ala	Ile	Pro	Leu	Ile	Leu	Ser	Thr	Gln	Val	Val	Val
					180			185				190			
Asp	Gly	Lys	Lys	Thr	Val	Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Lys	Thr	Leu
					195			200			205				
Lys	Pro	Ala	Ala	Ala	Arg	Lys	Phe	Glu	Pro	Ala	Ser	Leu	Thr	Ala	Gly
					210			215			220				

Glu Ser Val Gly Ile Val Arg Phe Leu Met Leu Glu Lys Pro Thr Pro
 225 230 235 240
 Glu Ile Ile Asn Ala Ile Glu Ser Ala Ile Ala Trp Tyr Lys Ala Asn
 245 250 255
 Asn Ile Ser Gly Leu Arg Trp Glu Arg Arg Asn Gly Glu Asn Ile Val
 260 265 270
 Ile Lys Asp Lys Asn Ala Pro Pro Val Trp Ala Arg Phe Tyr Gln Ile
 275 280 285
 Glu Thr Met Arg Pro Ile Phe Ala Gly Arg Asp Ala Val Ile Arg Tyr
 290 295 300
 Asp Val Met Gln Ile Glu Ser Glu Arg Arg Asn Gly Tyr Ala Trp Tyr
 305 310 315 320
 Val Ser Glu Pro Asn Glu Leu Leu Asn Glu Asp Tyr Pro Lys Trp Arg
 325 330 335
 Thr Arg Ser Ala Lys Arg Ala Gln Ile Phe Gln Arg Pro Pro Leu Gly
 340 345 350
 Ser Arg Phe Arg Thr Val
 355

<210> 7

<211> 1125

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 7

gtgcatgcgg	gccccggaaaca	cgtgagccga	tggcgccaaag	agtttcctgcg	cgacttcggcc	60
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ccggccggcga	tccgctgggg	agcggacgtc	ctgcggcaga	agccggagtg	gtatgcctcg	180
cgagaggcga	ggacgatcgc	cgacagcgtc	atccagtacc	aggccggcga	cgccggctgg	240
ccccagaaca	ccgaccctcgg	gactccggcc	acggctgaat	cacgcgcccc	cgcggcgccc	300
gacgtgacgt	cgagcacatt	cgacacaacaac	ggcacacgca	tgccgatgca	gttccttgcg	360
ctgggtggcg	acgcgaccgg	cgaggctcgc	tatcgcgcgt	cgttcctccg	cggttcgcac	420
tacctgctcg	ccgcgcagta	tcccaacggc	ggctggccgc	agttctttcc	gtccgcgcgc	480
gggttattaca	cccacatcac	cttcaacgac	aacgcgatgg	tcaacgtgt	gaccgtgtcg	540
cgcgatccg	cgcccggtca	ggcccccatac	gccttcgtgg	acgagccccg	ccgcgcgaag	600
gcccgcgcg	ccgtgtcccg	ggggatcga	gtcatcctga	agacccaaatg	gaaacagaac	660
ggcaagctga	cggcgtggtg	cgcgcagcac	gacgagaaga	ccctcgccgc	ggcgtggcg	720
cgcgcttacg	agccgcctac	gtctccggc	agcgaaccg	tcggcatcg	ccgcttcctg	780
atggagatcg	agaagccgtc	accggagatc	gtcgccgcga	tcaagggggc	cgtcgcctgg	840
ctgaagtccg	tggcgattcc	ggggctgcgc	tacgactcct	tcaccggcgc	ggacggacag	900
agggaccgccc	gcgtcggtcc	ggatccatcg	gcccggactcc	tgtgggcgcg	gttctacgag	960
ctcggcacca	accggccat	cttcctcgcc	cgcgactccg	ttgttcgcgc	cgcgctcagt	1020
gacatcgaac	gcgagcgccc	cgcggctac	gcctactacg	gtacgtggcc	ggcgagcctg	1080
attgctgcgg	actaccgcg	ctggcggtcg	acgctccggc	gctga		1125

<210> 8

<211> 374

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(374)

<223> Catalytic domain

<400> 8

Met His Ala Gly Ala Lys His Val Ser Arg Trp Arg Glu Glu Phe Leu
 1 5 10 15

Arg Asp Phe Ala Ala Arg Leu Ser Arg Thr Ile Pro Ser Ser Pro Ala
 20 25 30

Gln Ser Ala Ala Val Ser Gly Val Pro Ala Ala Ile Arg Trp Gly Ala
 35 40 45

Asp Val Leu Arg Gln Lys Pro Glu Trp Tyr Ala Ser Arg Glu Ala Arg
 50 55 60

Thr Ile Ala Asp Ser Val Ile Gln Tyr Gln Ala Ala Asp Gly Gly Trp
 65 70 75 80

Pro Lys Asn Thr Asp Leu Gly Thr Pro Pro Thr Ala Glu Ser Arg Ala
 85 90 95

Gly Ala Ala Ala Asp Val Thr Ser Ser Thr Ile Asp Asn Asn Gly Thr
 100 105 110

Thr Met Pro Met Gln Phe Leu Ala Leu Val Ala Asp Ala Thr Gly Glu
 115 120 125

Ala Arg Tyr Arg Ala Ser Phe Leu Arg Gly Phe Asp Tyr Leu Leu Ala
 130 135 140

Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Phe Phe Pro Leu Arg Arg
 145 150 155 160

Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asn Ala Met Val Asn Val
 165 170 175

Leu Thr Val Leu Arg Asp Ala Ala Gly Gln Ala Pro Tyr Ala Phe
 180 185 190

Val Asp Glu Pro Arg Arg Ala Lys Ala Arg Ala Ala Val Ser Arg Gly
 195 200 205

Ile Asp Val Ile Leu Lys Thr Gln Val Lys Gln Asn Gly Lys Leu Thr
 210 215 220

Ala Trp Cys Ala Gln His Asp Glu Lys Thr Leu Ala Pro Ala Trp Ala
 225 230 235 240

Arg Ala Tyr Glu Pro Pro Ser Leu Ser Gly Ser Glu Thr Val Gly Ile
 245 250 255

Val Arg Phe Leu Met Glu Ile Glu Lys Pro Ser Pro Glu Ile Val Ala
 260 265 270

Ala Ile Glu Gly Ala Val Ala Trp Leu Lys Ser Val Ala Ile Pro Gly
 275 280 285

Leu Arg Tyr Glu Ser Phe Thr Gly Ala Asp Gly Gln Arg Asp Arg Arg
 290 295 300

Val Val Pro Asp Pro Ser Ala Gly Leu Leu Trp Ala Arg Phe Tyr Glu
 305 310 315 320

Leu Gly Thr Asn Arg Pro Ile Phe Leu Gly Arg Asp Ser Val Val Arg
 325 330 335

Ala Ala Leu Ser Asp Ile Glu Arg Glu Arg Arg Ala Gly Tyr Ala Tyr
 340 345 350

Tyr Gly Thr Trp Pro Ala Ser Leu Ile Ala Ala Asp Tyr Pro Arg Trp
 355 360 365

Arg Ser Thr Leu Arg Arg
 370

<210> 9

<211> 1116

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 9

ttgatcggt	gcatgaaaac	gattctctca	aatctgaacg	cgccgctgct	ttcatgcgcc	60
ctgcttttgc	cgccagccac	acaggaaacc	aagcccccgg	aagtgcggtg	gaatgagtgc	120
ctaaacccaa	aacctgcctg	gtacggcagc	ccggaagcgg	tgcgcattgc	tgacaacctg	180
ttgcttacc	aacgcgacca	cgccggctgg	cacaagaata	tcgaaatggc	tgcggcttg	240
accgaacagc	aacaggcaga	gttcaaagcg	caaaaggcaa	ccgacgattc	gacgattgat	300
aacggcgcga	cctataccca	gtgttattat	ctggcgcgcg	tcttcaatgc	gacgaaggag	360
gagcgattca	aaaccgcgtt	tctcaaaggaa	ttcgattatc	tgctcaaggc	tcagttatcg	420
aacggcggct	ggccgcagta	ttacccgcgt	ttgcagggtt	attacaaaca	catcacgttc	480
aacgatgacg	cgatggctgg	cgtgttgcgt	tttctgcgcg	atgttgcgcg	cgccgattcc	540
ggttatcggt	tcgtggacag	cgaccggcgc	gcccgcgc	gccaggccgt	gcaaaaagga	600
attgagtgca	tcttggaaatg	ccagatcg	gtcggcggga	aaaagaccgc	ctggcgcgc	660
caacacgatg	aagtgcacatt	cgcccccgcg	ccggcacgca	cctacgagaa	aatttcgcgt	720
agccgcagcg	aatcgggttgg	cctgatccgc	ttcctgatgg	gcattgaaca	accggacgcg	780
cgtgttagttg	aggcgattga	gtccggcgtt	gcctggctca	agcaaggccaa	gctgaccggc	840
atcaaagtgg	ttcagaaggc	gatgttgcgt	aagcccaatg	gcttcgaccg	ggtcgtcg	900
gaagatgcac	aagccgggccc	attgtggggc	cgcttttacg	agatcggtac	gggcccgc	960
atctttccg	gacgtgacgg	catcgtaaa	tacagcttgg	cgaaatcga	acacgaacgg	1020
cgcacgggct	acggctggta	cacgaatgcg	cccgcaaat	tgctgaaaca	agattatccg	1080
gcctggcaaa	tcaaaccgcgg	gggcaagaaa	aagtaa			1116

<210> 10

<211> 371

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(29)

<221> DOMAIN

<222> (30)...(371)

<223> Catalytic domain

<400> 10

Met	Ile	Gly	Ser	Met	Lys	Thr	Ile	Leu	Ser	Asn	Leu	Asn	Ala	Ala	Leu
1				5				10				15			
Leu	Ser	Cys	Ala	Leu	Leu	Phe	Ala	Ala	Ala	Thr	Gln	Gly	Thr	Lys	Pro
				20				25				30			
Pro	Glu	Val	Arg	Trp	Asn	Glu	Cys	Leu	Asn	Gln	Lys	Pro	Ala	Trp	Tyr
				35				40			45				
Gly	Ser	Pro	Glu	Ala	Val	Arg	Ile	Ala	Asp	Asn	Leu	Leu	Tyr	Gln	
				50				55			60				
Arg	Asp	His	Gly	Gly	Trp	His	Lys	Asn	Ile	Glu	Met	Ala	Ala	Val	Leu
					65			70		75		80			
Thr	Glu	Gln	Gln	Ala	Glu	Leu	Lys	Ala	Gln	Lys	Ala	Thr	Asp	Asp	
					85			90			95				
Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Tyr	Thr	Gln	Val	Ile	Tyr	Leu	Ala
					100			105				110			
Arg	Val	Phe	Asn	Ala	Thr	Lys	Gln	Glu	Arg	Phe	Lys	Thr	Ala	Phe	Leu
					115			120			125				
Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Tyr	Ala	Asn	Gly	Gly	Trp
					130			135			140				
Pro	Gln	Tyr	Tyr	Pro	Arg	Leu	Gln	Gly	Tyr	Tyr	Lys	His	Ile	Thr	Phe
					145			150		155			160		
Asn	Asp	Asp	Ala	Met	Val	Gly	Val	Leu	Asp	Leu	Leu	Arg	Asp	Val	Ala
					165			170			175				

Arg Gly Asp Ser Gly Tyr Arg Phe Val Asp Ser Asp Arg Arg Ala Arg
 180 185 190
 Ala Ser Gln Ala Val Gln Lys Gly Ile Glu Cys Ile Leu Lys Cys Gln
 195 200 205
 Ile Val Val Ala Gly Lys Lys Thr Ala Trp Cys Ala Gln His Asp Glu
 210 215 220
 Val Thr Phe Ala Pro Ala Pro Ala Arg Thr Tyr Glu Lys Ile Ser Leu
 225 230 235 240
 Ser Gly Ser Glu Ser Val Gly Leu Ile Arg Phe Leu Met Gly Ile Glu
 245 250 255
 Gln Pro Asp Ala Arg Val Val Glu Ala Ile Glu Ser Ala Val Ala Trp
 260 265 270
 Leu Lys Gln Ala Lys Leu Thr Gly Ile Lys Val Val Gln Lys Ala Asp
 275 280 285
 Ala Ser Lys Pro Asn Gly Phe Asp Arg Val Val Val Glu Asp Ala Gln
 290 295 300
 Ala Gly Pro Leu Trp Ala Arg Phe Tyr Glu Ile Gly Thr Gly Arg Pro
 305 310 315 320
 Ile Phe Ser Gly Arg Asp Gly Ile Val Lys Tyr Ser Leu Ala Glu Ile
 325 330 335
 Glu His Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Thr Asn Ala Pro Ala
 340 345 350
 Lys Leu Leu Glu Gln Asp Tyr Pro Ala Trp Gln Ile Lys Arg Gly Gly
 355 360 365
 Lys Lys Lys
 370

<210> 11

<211> 1167

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 11
 atgtcggtgg gaccaggtgc taatccgaaa gtcgcgttc cctggtccaa acaactatcg 60
 ggtgttggg caaagttgtt cgatcgcgag cggttttca gcctcgctgc ggaacgaacc 120
 tctaaagaaga atgaccagca agtcggcgcc atcgctggaa aagatgcaca cggaaaggca 180
 gatgagtgggt atgcgagcgt tgaggcactt cgtatacgccg ataacgtcg tttctatcaa 240
 cgtgactcag gtggctggcc caaagatatac gagatggcga agacgttgag cgatcgtag 300
 aaggctgcga ttctccgcga gaagaaaaag aatgactcaa caatcgacaa tggcgcgact 360
 cacactcagt tatctttctt ggcgcgcgtc tatacagcac aacagcgagga gcgacatcgc 420
 gagtcatttt taaaaggact ggattactta ctgaaggcgc agtattcaaa tggtggtctgg 480
 ccacagttct atccaaactt gaatggctac tacaacggta tcacgtacaa cgatggcgcg 540
 atgatcggtg tcatggact tctgcgtgat gttgcggcag cggaaacctga atacgcgttt 600
 gtcgatggaa ctcggcggtgc gaaggctgcg aacgcgggtgg aaaaaggcat cgtgtgcatt 660
 ttgaaaacgc aggtgggtgt tcatggggcgt cgcactgttt ggtgtgcaca acacgacgaa 720
 gtgacgtttt cggccgcgc tcaagaaag tttgagttt cttcggttag cggcggttag 780
 agcgtcgata ttgttcgatt tctaattgtcg ataaaggatc catcgctaa cgtgggtgaa 840
 tcgattgaat cggcagttaa atggttttag cagtccggcgc taaaaggcgt taagtgggtc 900
 aagaaaaaccg acgctactca acctaattggg ttcgattgtc tcgttggtaa agatccggag 960
 agtctgttt gggcgcgctt ttacgagatt ggcacaaacc gcccgttgc tgccggcggt 1020
 gatggagtgc ctaagtatga cgtcgccgcg atcgaacacg agcgcacgaaac gggttacgaa 1080
 tggtagttt atgaggcagc aaaactgtctg aaaaagatt atccggcggtg gaagaaacgaa 1140
 catgtcgta cgcacgcgt tcattag 1167

<210> 12

<211> 388

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(388)

<223> Catalytic domain

<400> 12

Met	Ser	Leu	Gly	Pro	Gly	Ala	Asn	Pro	Lys	Ala	Arg	Val	Pro	Trp	Ser
1				5					10					15	
Lys	Gln	Leu	Ser	Gly	Val	Glu	Ala	Lys	Leu	Phe	Asp	Arg	Glu	Arg	Phe
					20				25					30	
Phe	Ser	Leu	Ala	Ala	Glu	Arg	Thr	Ser	Lys	Lys	Asn	Asp	Gln	Gln	Val
					35				40					45	
Gly	Ala	Ile	Ala	Trp	Lys	Asp	Ala	His	Gly	Lys	Ala	Asp	Glu	Trp	Tyr
					50				55					60	
Ala	Ser	Val	Glu	Ala	Leu	Arg	Ile	Ala	Asp	Asn	Val	Val	Phe	Tyr	Gln
					65				70					80	
Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Glu	Met	Ala	Lys	Thr	Leu
					85				90					95	
Ser	Asp	Arg	Glu	Lys	Ala	Ala	Ile	Leu	Arg	Glu	Lys	Lys	Asn	Asp	
					100				105					110	
Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	His	Thr	Gln	Leu	Ser	Phe	Leu	Ala
					115				120					125	
Arg	Val	Tyr	Thr	Ala	Gln	Gln	Glu	Arg	His	Arg	Glu	Ser	Phe	Leu	
					130				135					140	
Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Tyr	Ser	Asn	Gly	Gly	Trp
					145				150					155	
Pro	Gln	Phe	Tyr	Pro	Asn	Leu	Asn	Gly	Tyr	Tyr	Lys	Arg	Ile	Thr	Tyr
					165				170					175	
Asn	Asp	Gly	Ala	Met	Ile	Gly	Val	Met	Lys	Leu	Leu	Arg	Asp	Val	Ala
					180				185					190	
Ala	Ala	Lys	Pro	Glu	Tyr	Ala	Phe	Val	Asp	Glu	Thr	Arg	Arg	Ala	Lys
					195				200					205	
Ala	Ala	Asn	Ala	Val	Glu	Lys	Gly	Ile	Val	Cys	Ile	Leu	Lys	Thr	Gln
					210				215					220	
Val	Val	Val	Asp	Gly	Arg	Arg	Thr	Val	Trp	Cys	Ala	Gln	His	Asp	Glu
					225				230					235	
Val	Thr	Phe	Ala	Pro	Ala	Pro	Ala	Arg	Lys	Phe	Glu	Leu	Ala	Ser	Leu
					245				250					255	
Ser	Gly	Gly	Glu	Ser	Val	Asp	Ile	Val	Arg	Phe	Leu	Met	Ser	Ile	Lys
					260				265					270	
Asp	Pro	Ser	Arg	Asn	Val	Val	Glu	Ser	Ile	Glu	Ser	Ala	Val	Lys	Trp
					275				280					285	
Phe	Glu	Gln	Ser	Glu	Leu	Lys	Gly	Val	Lys	Trp	Val	Lys	Lys	Thr	Asp
					290				295					300	
Ala	Thr	Gln	Pro	Asn	Gly	Phe	Asp	Cys	Val	Val	Val	Lys	Asp	Pro	Glu
					305				310					315	
Ser	Ser	Val	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile
					325				330					335	
Phe	Ala	Gly	Arg	Asp	Gly	Val	Pro	Lys	Tyr	Asp	Val	Ala	Gln	Ile	Glu
					340				345					350	
His	Glu	Arg	Arg	Thr	Gly	Tyr	Glu	Trp	Tyr	Val	Asp	Glu	Ala	Ala	Lys
					355				360					365	
Leu	Leu	Lys	Lys	Asp	Tyr	Pro	Ala	Trp	Lys	Lys	Arg	His	Val	Val	Thr
					370				375					380	

Thr Arg Val His
385

<210> 13
<211> 1065
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 13

atgaaaacga	tcagccttat	ttgcctcgca	atctctgctg	ggattctgga	ttcggttg	60
gcggcacgct	ggaacgaatt	cgcccagaag	gcggatgatt	gttatcgagg	tgacgaaggc	120
aggcgcttg	cttgcataat	tcttctcac	caatcaactgc	aaggaagctg	gcccaagaat	180
accgatacca	cccgagatt	cttcaatgga	gatctagcga	agattcaggg	cacgttcgac	240
aacggtgcg	cgacggacga	gttgcgttgc	ctggccgcg	cgtttgcgc	cacaaagaa	300
aaaaactacg	agtca	ccgaaaaggc	ttcgaacaca	ttctcgccgc	gcaatacgcg	360
aacggcgat	ggcccaata	ttcgcgcgc	cccaaagg	accaccgaca	cattaccttc	420
aacgataatt	cgatgtgcg	gctgatgatt	ttccttcgcg	aggtcacac	ttcaatctc	480
tactcgttcg	tcgaagcgc	gctgcgaaca	caagccgcg	aaagttcga	tcgcgtgt	540
cggtgattc	ttaagtgc	gatcgtcg	aacgggcaca	agaccgcgt	gtgcgcgca	600
catgatgaaa	cggatttcag	cccccgatcc	gcgctgtt	acgaaactgc	ttcgtcg	660
gttctgaat	cagtccgt	tgtgcgttgc	ctgatgagcc	tcgatcagcc	gagccgcg	720
gtgatcgat	ccatcacca	cgccgtagcg	tggttcgaat	cgccgaaagct	gcccggatc	780
aaaaccgttc	aagagaccga	tccgaattcg	cccaaaggct	ggaatcgcgt	cgtcgtaaaa	840
gatgaaatg	cccgaccgat	gtggcgcgt	ttctacgaca	tcaacaccaa	caaaccgttc	900
ttttgtgatc	gcgatgggt	gccaaaggcg	agtcttgcg	agatcggtt	tgaacggcgg	960
aacggttatg	cgtggctcg	atactggct	gaagacttgc	tcgcaagaga	gtatccagcg	1020
tggaaagatga	agtggctgaa	gccccaaagag	cgcccaagcat	tttga		1065

<210> 14
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<221> DOMAIN
<222> (23)...(354)
<223> Catalytic domain

<400> 14

Met	Lys	Thr	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Ser	Ala	Gly	Ile	Leu
1					5			10						15	
Asp	Ser	Val	Ala	Ala	Ala	Arg	Trp	Asn	Glu	Phe	Ala	Gln	Lys	Ala	Asp
						20		25					30		
Asp	Trp	Tyr	Arg	Gly	Asp	Glu	Gly	Arg	Arg	Val	Ala	Ser	Asn	Ile	Leu
					35		40			45					
Ser	His	Gln	Ser	Leu	Gln	Gly	Ser	Trp	Pro	Lys	Asn	Thr	Asp	Thr	Thr
					50		55			60					
Ala	Arg	Phe	Phe	Asn	Gly	Asp	Leu	Ala	Lys	Ile	Gln	Gly	Thr	Phe	Asp
65						70			75				80		
Asn	Gly	Ala	Thr	Thr	Asp	Glu	Leu	Arg	Phe	Leu	Ala	Arg	Ala	Phe	Val
					85			90					95		

Ala Thr Lys Glu Lys Asn Tyr Glu Ser Ala Phe Arg Lys Gly Phe Glu
 100 105 110
 His Ile Leu Ala Ala Gln Tyr Ala Asn Gly Gly Trp Pro Gln Tyr Ser
 115 120 125
 Pro Pro Pro Lys Ser Tyr His Arg His Ile Thr Phe Asn Asp Asn Ser
 130 135 140
 Met Val Arg Leu Met Ile Phe Leu Arg Glu Val Thr Thr Ser Asn Leu
 145 150 155 160
 Tyr Ser Phe Val Glu Ala Pro Leu Arg Thr Gln Ala Arg Glu Ser Phe
 165 170 175
 Asp Arg Gly Val Arg Cys Ile Leu Lys Cys Gln Ile Val Val Asn Gly
 180 185 190
 His Lys Thr Ala Trp Cys Ala Gln His Asp Glu Thr Asp Phe Ser Pro
 195 200 205
 Arg Ser Ala Arg Ser Tyr Glu Leu Pro Ser Leu Ser Gly Ser Glu Ser
 210 215 220
 Val Gly Ile Val Arg Leu Leu Met Ser Leu Asp Gln Pro Ser Arg Gly
 225 230 235 240
 Val Ile Asp Ala Ile Thr Asn Ala Val Ala Trp Phe Glu Ser Ala Lys
 245 250 255
 Leu Pro Gly Ile Lys Thr Val Gln Glu Thr Asp Pro Asn Ser Pro Lys
 260 265 270
 Gly Trp Asn Arg Val Val Val Lys Asp Glu Ser Ala Arg Pro Met Trp
 275 280 285
 Ala Arg Phe Tyr Asp Ile Asn Thr Asn Lys Pro Phe Phe Cys Asp Arg
 290 295 300
 Asp Gly Val Pro Lys Pro Ser Leu Ala Glu Ile Gly Tyr Glu Arg Arg
 305 310 315 320
 Asn Gly Tyr Ala Trp Leu Gly Tyr Trp Pro Glu Asp Leu Leu Ala Arg
 325 330 335
 Glu Tyr Pro Ala Trp Lys Met Lys Trp Leu Lys Pro Lys Glu Arg Pro
 340 345 350
 Ala Phe

<210> 15
 <211> 1575
 <212> DNA
 <213> Bacteria

<400> 15
 atgagacgac cagtcgcact ccggctccac gcggcactgg ccaccctggc cctggcgcc 60
 gcgaccggcg tggtgctctc gatcccccaq gcatcgccgg cggccggcg cgccaccggc 120
 tacgcccccc agaacggcg caccacggc ggtccggcg gccagaccgt acggggccacc 180
 acggggcaccg ccatccacgc gcccctgtgc ggacgggcca gcagcagcac cccgatcacg 240
 atcgaggtcg agggAACGAT caaccacgccc aacaccggca aggtgtccgg ccccaagctgc 300
 aacaccggcg ccggagtgat cgagctgaag cagatcagca acgtcacgct cgtccccgtc 360
 ggctccggcg cctgtttcg acaactcgcc atccacatcc gcgagttccag caacatcatc 420
 atccagaacg tgacggtccg gaacgtcaag aagtccggct cggcgctgtc caacggcgcc 480
 gacgccccatcg gcatggagag cgacgtccgc aacgtctggg tcgaccactc caccctggag 540
 gcctccggcg gcgagttccg aggctacgac ggcctttcg acatgaagga caacaccgg 600
 tacgtgaccc tgcgtacag catcctgcgc aaatccggc gggccggcct cgtggggtcc 660
 agcgagaccc aactctcgaa cagttcattc acgttaccacc acaacctgtt cggaaacatc 720
 gactcgcgcg cggccctgtct ggcggccggg accgcccaca tgtacaacaa ccactacctg 780
 cggatcaacg agtccggcat caactcccgat gccggagccc acgccaaggt ggacaacaac 840
 tacttcgagg actccaagga cgtcctcgcc accttctaca cccgacggccg cgggtactgg 900
 caggtcagcg gcaacgtcta cgacaacgtg acctggtccg cccggggcac cgacaacaac 960
 cggccggggc cggaccggca gtcacaacacc accgtctcca tcccctacgc cttcagcctc 1020
 gacccggcca cctgcgtgcc ggacgtcgtg agccgaacgg cgggtccgg caagggactt 1080

caggtgtcga acggcagctg ctccccgca	1140
accacacccg cgccgacgac tcccaccccg	1200
cagcccggcg ggacgaacct cagcatcggt	1260
ggcaccagct acggcaacgt cggggacggg	1320
tcgaccggct ccgtgtcgat caagtgggc	1380
cgcgaggcgg cggcgac gggcgtcatt	1440
ggcgcgtgc tgacctccgg cagcggggcg	1500
aagaagatca ctttcgagat cacgggacgc	1560
acgtacgccc gctag	1575

<210> 16
<211> 524
<212> PRT
<213> Bacteria

<220>

<221> SIGNAL
<222> (1)...(33)

<221> DOMAIN
<222> (34)...(359)
<223> Catalytic domain

<400> 16	
Met Arg Arg Pro Val Ala Leu Arg Leu His Ala Ala Leu Ala Thr Leu	
1 5 10 15	
Ala Leu Ala Ala Ala Thr Gly Val Val Leu Ser Ile Pro Gln Ala Ser	
20 25 30	
Ala Ala Ala Gly Gly Ala Thr Gly Tyr Ala Gly Gln Asn Gly Gly Thr	
35 40 45	
Thr Gly Gly Ala Gly Gly Gln Thr Val Arg Ala Thr Thr Gly Thr Ala	
50 55 60	
Ile His Ala Ala Leu Cys Gly Arg Ala Ser Ser Ser Thr Pro Ile Thr	
65 70 75 80	
Ile Glu Val Glu Gly Thr Ile Asn His Ala Asn Thr Ala Lys Val Ser	
85 90 95	
Gly Pro Ser Cys Asn Thr Ala Ala Gly Val Ile Glu Leu Lys Gln Ile	
100 105 110	
Ser Asn Val Thr Leu Val Gly Val Gly Ser Gly Ala Val Phe Asp Gln	
115 120 125	
Leu Gly Ile His Ile Arg Glu Ser Ser Asn Ile Ile Ile Gln Asn Val	
130 135 140	
Thr Val Arg Asn Val Lys Lys Ser Gly Ser Pro Leu Ser Asn Gly Gly	
145 150 155 160	
Asp Ala Ile Gly Met Glu Ser Asp Val Arg Asn Val Trp Val Asp His	
165 170 175	
Ser Thr Leu Glu Ala Ser Gly Gly Glu Ser Glu Gly Tyr Asp Gly Leu	
180 185 190	
Phe Asp Met Lys Asp Asn Thr Arg Tyr Val Thr Leu Ser Tyr Ser Ile	
195 200 205	
Leu Arg Lys Ser Gly Arg Gly Gly Leu Val Gly Ser Ser Glu Thr Glu	
210 215 220	
Leu Ser Asn Ser Phe Ile Thr Tyr His His Asn Leu Tyr Glu Asn Ile	
225 230 235 240	
Asp Ser Arg Ala Pro Leu Leu Arg Gly Gly Thr Ala His Met Tyr Asn	
245 250 255	
Asn His Tyr Leu Arg Ile Asn Glu Ser Gly Ile Asn Ser Arg Ala Gly	
260 265 270	

Ala His Ala Lys Val Asp Asn Asn Tyr Phe Glu Asp Ser Lys Asp Val
 275 280 285
 Leu Gly Thr Phe Tyr Thr Asp Ala Ala Gly Tyr Trp Gln Val Ser Gly
 290 295 300
 Asn Val Tyr Asp Asn Val Thr Trp Ser Ala Arg Gly Thr Asp Asn Asn
 305 310 315 320
 Pro Ala Gly Pro Asp Pro Gln Ser Asn Thr Thr Val Ser Ile Pro Tyr
 325 330 335
 Ala Phe Ser Leu Asp Pro Ala Thr Cys Val Pro Asp Val Val Ser Arg
 340 345 350
 Thr Ala Gly Ala Gly Lys Gly Leu Gln Val Ser Asn Gly Ser Cys Ser
 355 360 365
 Pro Gln Thr Pro Thr Pro Thr Pro Thr Gly Thr Pro Thr Thr Pro Ala
 370 375 380
 Pro Thr Thr Pro Thr Pro Ser Pro Thr Pro Ser Thr Pro Gly Pro Thr
 385 390 395 400
 Gln Pro Gly Gly Thr Asn Leu Ser Ile Gly Ala Gly Ser Asp Gly Ser
 405 410 415
 Ser Lys Ala Asp Gly Thr Ser Tyr Gly Asn Val Arg Asp Gly Asp Leu
 420 425 430
 Gly Thr His Trp Ser Pro Ala Gly Ser Thr Gly Ser Val Ser Ile Lys
 435 440 445
 Trp Gly Ser Ala Thr Thr Val Ser Arg Ile Val Ile Arg Glu Ala Ala
 450 455 460
 Gly Ala Thr Gly Val Ile Gly Ser Trp Leu Val Leu Asn Gly Asp Thr
 465 470 475 480
 Gly Ala Val Leu Thr Ser Gly Ser Gly Ala Gly Thr Ile Ser Val Pro
 485 490 495
 Arg Thr Ala Leu Lys Lys Ile Thr Phe Glu Ile Thr Gly Ala Ser Gly
 500 505 510
 Thr Pro Arg Ile Ala Glu Phe Glu Thr Tyr Ala Gly
 515 520

<210> 17
 <211> 1047
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 17

ttgccgcgtg	cgccccgtgg	ttagtcgtca	tcgcccagcgc	agacgtcatac	ggttgcggtc	60
tcctgggatc	agatcctccg	tcaagcctgctg	gcctggtagc	gcccgtcgaa	ggcgttgcga	120
gtcgctgaga	acgtgctctt	gtatcagcgc	gcccgcaggag	ggtggccgaa	gaacatcaac	180
atggcggcgc	cgatgaccgc	cgctgaccgt	gcaaaagtca	cggacgagcg	cgcgcagaac	240
gacgccacga	tgcacaacac	gtcaacgacg	acgcagatcc	gttttcttgc	gctcgttctt	300
cgccgcaccg	ccgacgcacg	attcaaggac	gcccgcgtga	agggcatcga	cttcctgctg	360
gctgcgcaat	acgcgaatgg	aggctggct	cagtatttc	ccctgcgcga	cgactactcg	420
cggcgcatac	cgttcaatga	cgacgcgtatc	gtaatgtga	tgacgtctgt	gcccgcgcgt	480
tcgcagggcc	agacgcgtt	cgagttcgtc	gacgcctcgc	ggcgcggccg	ggcggcgcag	540
tctgtctcac	gcccgcgtca	cgtcatgtc	cgcacgcaga	ttcgagtcaa	cggcgtgctg	600
acccgctggt	gccagcagca	cgacgcgcgg	aacttcagc	cggtgaaggc	gcccgcgtac	660
gaacatccgt	cgattgccag	caaggaaacc	gcccgcgtac	caagattcc	gatggggatt	720
gaacggccgt	cgccggagat	cgatgtccgc	gtggatggcg	cagtgcgtg	gttgcgcgcg	780
gcccgcgtt	cagggtgtcg	gacggagcgc	cgcccgcacg	gatcgaatcc	gggcggcgcac	840
gtcgtggcgg	tgcaggactc	cgccgcgcgg	ccaatctgg	cccgcgttcta	cgagattggc	900
accaaccggc	cgatgttttc	gggtcgcgac	ggcgtcatca	agtacagcct	cagcgcagatc	960
gagatcgagc	ggcgcgcgtgg	atacagctgg	tacggcgtact	acgcgcgcacg	actgctcaga	1020

gacgactatc cgaagtggaa gaaatga

1047

<210> 18
 <211> 348
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(348)
 <223> Catalytic domain

<400> 18
 Met Pro Arg Ala Pro Gly Gly Glu Ser Ser Ser Pro Ala Gln Thr Ser
 1 5 10 15
 Ser Val Ala Val Ser Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp
 20 25 30
 Tyr Gly Gly Ala Glu Ala Leu Arg Val Ala Glu Asn Val Leu Leu Tyr
 35 40 45
 Gln Arg Ala Ala Gly Gly Trp Pro Lys Asn Ile Asn Met Ala Ala Pro
 50 55 60
 Met Thr Ala Ala Asp Arg Ala Lys Val Thr Asp Glu Arg Ala Gln Asn
 65 70 75 80
 Asp Ala Thr Ile Asp Asn Thr Ser Thr Thr Gln Ile Arg Phe Leu
 85 90 95
 Ala Leu Val Leu Arg Gly Thr Ala Asp Ala Arg Phe Lys Asp Ala Ala
 100 105 110
 Leu Lys Gly Ile Asp Phe Leu Leu Ala Ala Gln Tyr Ala Asn Gly Gly
 115 120 125
 Trp Pro Gln Tyr Phe Pro Leu Arg Asp Asp Tyr Ser Arg Arg Ile Thr
 130 135 140
 Phe Asn Asp Asp Ala Met Val Asn Val Met Thr Leu Leu Arg Glu Thr
 145 150 155 160
 Ser Gln Gly Gln Thr Pro Phe Glu Phe Val Asp Ala Ser Arg Arg Gly
 165 170 175
 Arg Ala Ala Gln Ser Val Ser Arg Gly Val Asp Val Met Leu Arg Thr
 180 185 190
 Gln Ile Arg Val Asn Gly Val Leu Thr Gly Trp Cys Gln Gln His Asp
 195 200 205
 Glu Arg Asn Phe Gln Pro Val Lys Ala Arg Ala Tyr Glu His Pro Ser
 210 215 220
 Ile Ala Ser Lys Glu Thr Ala Ser Ile Ala Arg Phe Leu Met Gly Ile
 225 230 235 240
 Glu Arg Pro Ser Pro Glu Ile Val Ser Ala Val Asp Gly Ala Val Ala
 245 250 255
 Trp Leu Arg Ala Ala Gln Ile Ser Gly Val Arg Thr Glu Arg Arg Pro
 260 265 270
 Asp Gly Ser Asn Pro Gly Gly Asp Val Val Ala Val Gln Asp Ser Ala
 275 280 285
 Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro
 290 295 300
 Met Phe Ser Gly Arg Asp Gly Val Ile Lys Tyr Ser Leu Ser Glu Ile
 305 310 315 320
 Glu Ile Glu Arg Arg Ala Gly Tyr Ser Trp Tyr Gly Asp Tyr Ala Ala
 325 330 335
 Arg Leu Leu Arg Asp Asp Tyr Pro Lys Trp Lys Lys
 340 345

<210> 19
 <211> 1122
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 19

gtgaacagg	ggcgcaaga	cttcttgcgc	gacttcgcgg	cccgcatgt	ccgggtgc	60
gttccccggc	cgcatatcca	ctggggcggc	gggtgcatcc	ggcaggaaacc	ggaatggtac	120
ggctcgcccg	aggcgctgc	gatcgccgac	agcgcttcc	aataccagtc	gaccgctggc	180
ggctggccca	agaacaccga	cttgacggtc	tcgaccacgt	ccgccaatt	ccttgcggat	240
gcccgtggtc	tcacgaacac	gatcgacaac	gacgcacca	cggtgcgc	gcgatttctc	300
gctctggtgg	cgcacgcac	cggcggcattc	aagtaccgcg	ccgcgttcga	acgcggcttg	360
gactacctgc	tcgcccgtca	gtatccaaat	ggcggtggc	ctcagtttt	tccctgcgt	420
gacggctatt	actcgacat	cacccatacaac	gacaatgcga	ttgtcaacgt	cctcaccgtt	480
ctgcgcgtat	cgccgcggg	ccggcccccct	tactcggtcg	tcgacagggc	ccggcgcgccc	540
agagcagaaa	cggccatcgc	tcgcggcattc	gacatcatcg	tgcgcaactca	ggtgagacgg	600
gccccgtgc	tgaccgcatt	gtgcgcggc	cacgacgaaa	agacgctcg	ccggcgtgg	660
gcccccaact	acgaaccgc	gacactctcc	gggcacgaaa	gcgtcgcat	cgtcgcttt	720
ctcatggaa	tcgaaaagcc	cacgcggagg	atcgctcg	cggtgcaagg	cgccgctgac	780
tggttgagag	ccgtcgatc	cagcgggttg	cgtctcgagg	aattcaccga	cgccgatggc	840
aggcgcaca	ggcgcgtcg	cggcgatcc	gcagcgcgc	tcctgtggc	gcccgttac	900
gagcttggca	cgaccgtcc	cgtcttcacc	ggccgcgaca	aggtgatcc	gtactcgctc	960
agcgaatcg	agcacgagcg	coggaacggg	tatgcctact	atggcacatg	gccggccacg	1020
ctccctcagcg	aggagtaccc	cogttggcgc	gcgaaacacc	tggtcgacg	gagcgtcagg	1080
caggttagagg	agggaaatcgc	gatacgcgtc	cctaattccct	ga		1122

<210> 20
 <211> 373
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(373)
 <223> Catalytic domain

<400> 20

Met	Asn	Arg	Trp	Arg	Glu	Asp	Phe	Leu	Arg	Asp	Phe	Ala	Ala	Arg	Met
1				5				10				15			
Leu	Arg	Cys	Met	Val	Pro	Arg	Pro	Gln	Ile	His	Trp	Gly	Gly	Gly	Val
				20				25				30			
Ile	Arg	Gln	Glu	Pro	Glu	Trp	Tyr	Gly	Ser	Ala	Glu	Ala	Arg	Ala	Ile
				35			40				45				
Ala	Asp	Ser	Val	Leu	Gln	Tyr	Gln	Ser	Thr	Ala	Gly	Gly	Trp	Pro	Lys
				50			55				60				
Asn	Thr	Asp	Leu	Thr	Val	Ser	Pro	Pro	Ser	Ala	Glu	Phe	Leu	Ala	Asp
				65			70				75				80
Ala	Asp	Gly	Leu	Thr	Asn	Thr	Ile	Asp	Asn	Asp	Ala	Thr	Thr	Leu	Pro
				85			90				95				
Met	Arg	Phe	Leu	Ala	Leu	Val	Ala	His	Ala	Thr	Gly	Gly	Ile	Lys	Tyr
				100			105				110				
Arg	Ala	Ala	Phe	Glu	Arg	Gly	Leu	Asp	Tyr	Leu	Leu	Ala	Ala	Gln	Tyr
				115			120				125				

Pro Asn Gly Gly Trp Pro Gln Tyr Phe Pro Leu Arg Asp Gly Tyr Tyr
 130 135 140
 Ser His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Val
 145 150 155 160
 Leu Arg Asp Ala Ala Ala Gly Arg Pro Pro Tyr Ser Phe Val Asp Arg
 165 170 175
 Ala Arg Arg Ala Arg Ala Glu Thr Ala Ile Ala Arg Gly Ile Asp Ile
 180 185 190
 Ile Val Arg Thr Gln Val Arg Arg Ala Gly Val Leu Thr Ala Trp Cys
 195 200 205
 Ala Gln His Asp Glu Lys Thr Leu Glu Pro Ala Trp Ala Arg Asn Tyr
 210 215 220
 Glu Pro Pro Thr Leu Ser Gly His Glu Ser Val Gly Ile Val Arg Phe
 225 230 235 240
 Leu Met Gly Ile Glu Lys Pro Thr Pro Arg Ile Val Ala Ala Val Gln
 245 250 255
 Gly Ala Ala Asp Trp Leu Arg Ala Val Ala Ile Ser Gly Leu Arg Leu
 260 265 270
 Glu Glu Phe Thr Asp Ala Asp Gly Arg Arg Asp Arg Arg Val Val Ala
 275 280 285
 Asp Pro Ala Ala Pro Leu Leu Trp Ala Arg Phe Tyr Glu Leu Gly Thr
 290 295 300
 Asp Arg Pro Val Phe Thr Gly Arg Asp Lys Val Ile Arg Tyr Ser Leu
 305 310 315 320
 Ser Glu Ile Glu His Glu Arg Arg Asn Gly Tyr Ala Tyr Tyr Gly Thr
 325 330 335
 Trp Pro Ala Thr Leu Leu Ser Glu Glu Tyr Pro Arg Trp Arg Ala Lys
 340 345 350
 His Leu Ala Arg Arg Ser Val Arg Gln Val Glu Glu Gly Ile Ala Ile
 355 360 365
 Arg Val Pro Asn Pro
 370

<210> 21

<211> 1269

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 21

atgcgttaat cgaactgggc cgtcacaaacg	gcccattctgc tcgcgctgag	cgccgcaccg	60
ctggcgccaa agcccatcg	acagatcacc ctcgcgtgc	cgctcagccc ggccgcgc	120
accgaaacgc cgccctgagca	gcgggcgc	ttgcaggc	180
cagcttaagg cagacaaggc	ggcgctggc	gcccagcgc	240
gccaagccga agaccggc	cgcacacc	ccggctcg	300
atgcgcgtccg aggcgcgtct	ggtcgccc	acaagccgt	360
ggctggggca aaaatcaggc	gatatacgta	ggtatcagac	420
atcgatgacg ccgatccac	cggttcggc	tccggcaggc	480
gacgccacca tcgtggaaat	tcgtttctc	ggccgcgt	540
gaaggcgacg tctatcg	ctccgcac	cgccgc	600
taccccaatg gcccgtggc	gcaggctgg	ccgttcagg	660
accctcaatg acggcg	gtccatgt	gcccgtatca	720
caggcgact tcgccttc	gcctgagcc	cgacgc	780
aagggtcaga aggtgttct	cgatcttc	acggcgaacg	840
gcccgcgt	cttaa	caccctgtgg	900
tcgatcagca ccggtgaaag	cccagcgg	cgctgtaacta	960
tcgcctgaag tgcgcgacgc	catcgaaaaa	cgagccgtcg	1020

aacggcatgg	catggaaaaa	ggacggcatg	cgcaaacgtc	tggtcgccaa	ggctgacgcc	1080
tcgcccgtgt	ggtcgcgcta	tcacgactcg	gaaacgctgc	tgcccatctt	cggtgaccgc	1140
gacatgcgca	tcttcgacga	cgtcaacgac	atcagcgacg	aacgcagccg	cggctatgcc	1200
tggtatggca	caagccggc	acgggccatc	gccgaatacg	aaaaatggaa	acagggcaac	1260
ggcaaatga						1269

<210> 22
<211> 422
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(23)

<221> DOMAIN
<222> (24)...(422)
<223> Catalytic domain

<400> 22
Met Arg Lys Ser Asn Trp Ala Val Thr Thr Ala Ile Leu Leu Ala Leu
1 5 10 15
Ser Ala Ala Pro Leu Ala Ala Lys Pro Ile Gly Gln Ile Thr Leu Ala
20 25 30
Val Pro Leu Ser Pro Ala Arg Leu Thr Glu Thr Pro Pro Glu Gln Arg
35 40 45
Ala Gln Trp Gln Ala Tyr Leu Ala Thr Thr Glu Ala Gln Leu Lys Ala
50 55 60
Asp Lys Ala Ala Leu Ala Ala Glu Arg Ala Gly Leu Ala Glu Ile Pro
65 70 75 80
Ala Lys Pro Lys Thr Gly Ser Ala Asn Thr Met Pro Leu Asp Lys Pro
85 90 95
Leu Glu Trp Tyr Ala Ser Ser Glu Ala Arg Leu Val Ala Asp Asn Ile
100 105 110
Val Ser Tyr Gln Thr Pro Ala Gly Gly Trp Gly Lys Asn Gln Ala Arg
115 120 125
Asn Glu Pro Thr Arg Leu Lys Gly Gln Ala Tyr Thr Ile Asp Asp Ala
130 135 140
Asp Pro Thr Gly Ser Gly Lys Trp Asn Phe Val Gly Thr Ile Asp Asn
145 150 155 160
Asp Ala Thr Ile Val Glu Ile Arg Phe Leu Ala Arg Val Ala Ala Ala
165 170 175
Ala Thr Gly Pro Glu Gly Asp Val Tyr Arg Ala Ser Ala Thr Arg Gly
180 185 190
Ile Thr Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln
195 200 205
Val Trp Pro Leu Gln Gly Gly Tyr His Asp Ala Ile Thr Leu Asn Asp
210 215 220
Gly Ala Met Ile His Val Leu Glu Leu Phe Asp Asp Ile Ala Ser Gly
225 230 235 240
Gln Gly Asp Phe Ala Phe Leu Pro Glu Pro Leu Arg Asp Lys Val Glu
245 250 255
Ala Ala Gln Ala Lys Gly Gln Lys Val Leu Leu Asp Leu Gln Leu Lys
260 265 270
Arg Asn Gly Glu Arg Thr Leu Trp Ala Gln Gln Tyr Asp Pro Ile Thr
275 280 285
Leu Leu Pro Ser Ala Ala Arg Asn Tyr Glu Pro Ser Ser Ile Ser Thr

290	295	300													
Gly	Glu	Ser	Ala	Gly	Val	Leu	Ile	Tyr	Leu	Met	Ser	Leu	Pro	Asn	Pro
305					310					315					320
Ser	Pro	Glu	Val	Arg	Asp	Ala	Ile	Glu	Lys	Gly	Val	Ala	Leu	Leu	Ile
						325			330					335	
Lys	Leu	Gln	Ile	Asn	Gly	Met	Ala	Trp	Glu	Lys	Asp	Gly	Met	Arg	Lys
						340			345					350	
Arg	Leu	Val	Ala	Lys	Ala	Asp	Ala	Ser	Pro	Leu	Trp	Ser	Arg	Tyr	His
							355		360				365		
Asp	Ser	Glu	Thr	Leu	Leu	Pro	Ile	Phe	Gly	Asp	Arg	Asp	Met	Arg	Ile
						370		375			380				
Phe	Asp	Asp	Val	Asn	Asp	Ile	Ser	Asp	Glu	Arg	Ser	Arg	Gly	Tyr	Ala
						385		390		395				400	
Trp	Tyr	Gly	Thr	Ser	Pro	Ala	Arg	Ala	Ile	Ala	Glu	Tyr	Glu	Lys	Trp
						405			410					415	
Lys	Gln	Gly	Asn	Gly	Lys										
					420										

<210> 23

<211> 1182

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 23

atgaaccgtg	gcgtgattgt	tttgctggcg	gccgctccag	ctgcggcgca	tggcgcagtg	60
ctgggtata	tgacgcctgc	gcagccgttg	accgagggcgc	gcattgccgc	gctgccggcg	120
tcggagcagg	gcgcctggcg	ggctcacctc	gcccgtccc	gcgcaagccat	ggacgcccac	180
aaggccccc	tggcccccga	gcgcgcccgc	ctgcaccgc	taccgcccggc	gcccggccat	240
ggcgggtgg	atggcggat	ggcgcgcaac	cgtccgacgg	cttggtatgg	gacgcccggaa	300
gcgcggcaca	tcgcggacaa	tatcgtcagc	ttccagacgc	cgtccggcg	ctggggcaag	360
aacgtggacc	gcacgggacc	tgtgcggccag	cgcggacagc	attacgtttc	cttcgatggc	420
aaggagtcc	ggaacttcat	cgcacgatc	gacaacaacg	ccacaacgag	cgagctgaaa	480
ttctctggcgc	gcgtgcaggc	gcaaattgccc	ggcgcggcg	gcgacgaaata	ccggaaggcc	540
gcctctgcgc	gcatcagcta	cctgttgaac	tcacaatatc	ccaacggcg	cttcccgca	600
gtctatccgc	tgcaaggcg	ctaccacgac	gccatcacct	tcaacgacga	tgccttcg	660
aacgtgctgc	aagtgcgtct	ggaagtggcg	aaccgcagg	gcgactatgc	cttcgtcccc	720
gaaaccgtgg	caaccgatgc	ccgcgcggcc	gcccacaagg	cgctccaagt	cctgtggcg	780
agccagatca	tcgtcgccgg	cgtacgcacc	gcctggtgc	agcagcacga	tgcgatcacg	840
ctggcgcccc	tcggcgcccc	caatttcgaa	ccggccgcgc	tgaccagcac	ggaaagcg	900
cgctctgt	tgctgttgat	gctgctgccc	gatccgagcc	cggagctgag	agcgtcaatc	960
catgcgggaa	tggcttgct	gcagaaagcg	gcccgtccgg	ggatgtctg	gtcgcgctac	1020
tatgacctga	acacgatgag	gccgatctt	ggggatcg	accgcagtat	ccacgatgat	1080
gtgaaggaat	tgagcgagga	gaggcaaaaa	ggctatggct	ggttcagtaa	cggaccagcc	1140
agagctaaac	aggctttga	ggcctggacg	cgcaaacctt	ga		1182

<210> 24

<211> 393

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(18)

<221> DOMAIN

<222> (19)...(393)

<223> Catalytic domain

<400> 24

Met	Asn	Arg	Gly	Val	Ile	Val	Leu	Leu	Ala	Ala	Ala	Pro	Ala	Ala	Ala
1				5				10					15		
His	Gly	Ala	Val	Leu	Gly	Tyr	Met	Thr	Pro	Ala	Gln	Pro	Leu	Thr	Glu
				20				25					30		
Ala	Arg	Ile	Ala	Ala	Leu	Pro	Ala	Ser	Glu	Gln	Gly	Ala	Trp	Arg	Gly
				35				40				45			
Tyr	Leu	Ala	Arg	Ser	Arg	Ala	Ala	Met	Asp	Ala	Asp	Lys	Ala	Ala	Leu
				50				55			60				
Ala	Ala	Glu	Arg	Ala	Ala	Leu	Ala	Thr	Val	Pro	Pro	Ala	Pro	Pro	His
				65				70			75		80		
Gly	Gly	Gly	Asp	Gly	Gly	Met	Ala	Arg	Asn	Arg	Pro	Thr	Ala	Trp	Tyr
				85				90				95			
Gly	Thr	Pro	Glu	Ala	Arg	His	Ile	Ala	Asp	Asn	Ile	Val	Ser	Phe	Gln
				100				105				110			
Thr	Pro	Ser	Gly	Gly	Trp	Gly	Lys	Asn	Val	Asp	Arg	Thr	Gly	Pro	Val
				115				120				125			
Arg	Gln	Arg	Gly	Gln	His	Tyr	Val	Ser	Phe	Asp	Gly	Lys	Glu	Ser	Trp
				130				135			140				
Asn	Phe	Ile	Gly	Thr	Ile	Asp	Asn	Ala	Thr	Thr	Ser	Glu	Leu	Lys	
				145				150			155		160		
Phe	Leu	Ala	Arg	Val	Gln	Ala	Gln	Met	Pro	Gly	Ala	Ala	Gly	Asp	Glu
				165				170				175			
Tyr	Arg	Lys	Ala	Ala	Leu	Arg	Gly	Ile	Ser	Tyr	Leu	Leu	Asn	Ser	Gln
				180				185				190			
Tyr	Pro	Asn	Gly	Gly	Phe	Pro	Gln	Val	Tyr	Pro	Leu	Gln	Gly	Gly	Tyr
				195				200				205			
His	Asp	Ala	Ile	Thr	Phe	Asn	Asp	Asp	Ala	Phe	Ala	Asn	Val	Leu	Gln
				210				215			220				
Val	Leu	Leu	Glu	Val	Ala	Asn	Arg	Arg	Gly	Asp	Tyr	Ala	Phe	Val	Pro
				225				230			235		240		
Glu	Thr	Val	Ala	Thr	Asp	Ala	Arg	Ala	Ala	Asp	Lys	Ala	Leu	Gln	
				245				250				255			
Val	Leu	Leu	Ala	Ser	Gln	Ile	Ile	Val	Gly	Gly	Val	Arg	Thr	Ala	Trp
				260				265				270			
Cys	Gln	Gln	His	Asp	Ala	Ile	Thr	Leu	Ala	Pro	Val	Gly	Ala	Arg	Asn
				275				280			285				
Phe	Glu	Pro	Ala	Ala	Leu	Thr	Ser	Thr	Glu	Ser	Ala	Arg	Leu	Leu	Met
				290				295			300				
Leu	Leu	Met	Leu	Leu	Pro	Asp	Pro	Ser	Pro	Glu	Leu	Arg	Ala	Ser	Ile
				305				310			315		320		
His	Ala	Gly	Met	Ala	Trp	Leu	Gln	Lys	Ala	Ala	Leu	Pro	Gly	Asp	Val
				325				330				335			
Trp	Ser	Arg	Tyr	Tyr	Asp	Leu	Asn	Thr	Met	Arg	Pro	Ile	Phe	Gly	Asp
				340				345				350			
Arg	Asp	Arg	Ser	Ile	His	Asp	Asp	Val	Lys	Glu	Leu	Ser	Glu	Glu	Arg
				355				360				365			
Gln	Lys	Gly	Tyr	Gly	Trp	Phe	Ser	Asn	Gly	Pro	Ala	Arg	Ala	Lys	Gln
				370				375				380			
Ala	Phe	Glu	Ala	Trp	Thr	Arg	Lys	Pro							
				385				390							

<210> 25

<211> 1194

<212> DNA

File: 1C37.pdb

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 25

ttggtcgctg	ccctattaag	ctgcggcagc	gccaatctct	atgcagaatc	aaccgaaaaa	60
tcggcacgc	aatcagcagc	cacaatcaa	ttgcaaaatg	aaaaaaagcag	ttggacagc	120
tattacgccc	catccaaaaa	aatacatcag	gcagaccagg	attttctcgc	cgctgaatta	180
aaaaaaactcg	gtcagaaaaa	accaacattt	ccgcacaca	ccaaagattt	tggttttgat	240
gttaagcagg	taaatgcaga	ttggtttaaa	agtgcgaag	gcaaacgtgt	gatggagatt	300
attctctcct	tccaaacccc	gtccggcggt	tggtaaagc	gtaccgacat	ggccaaggcg	360
gtgcacaac	ctggcaagc	cttggcggt	gaaaaggct	atatcccaac	atttgataat	420
ggcgctacca	gcactcaatt	gatgttgctc	gchgcaagcac	accaagccac	cggcgatcac	480
cgttttagcg	acgcatttg	gchgccccgtt	caattaattt	tgactgcgca	atacccgaat	540
ggtggctggc	cacaactt	tccactaacc	ggtagctacc	acgattacat	cacccacaac	600
gacaatctt	cgcgcacact	gatggtagt	ctgcacaaaaa	cagcgcaggc	aaaaaatgtat	660
tttgcattcg	tgaccaaagc	gcagcaaattc	gcagcgtcag	ctagcctcgc	gcgtgcactt	720
gattgcgtat	tgaaatcaca	agttgtcg	aatggcacac	gcacacttgc	gggcccacag	780
cacgatgtta	aaacactgca	accaacccaa	gchgccccgt	ttgaaatgg	gtcaactcact	840
accactgaaa	gchgccccgt	gctcagttt	ctgtatggata	tcaaaaaatcc	cagcgcggat	900
attattcaat	ccatacatgc	agccatagcc	tggatgtgac	aaaataaaaat	cgtcgaaaaa	960
acctggacac	gtgggtatgc	ggaattaaaa	gataataaaa	attcgcagcc	actctggcg	1020
cgttttatg	agataggcac	taataagcct	atattgggg	atcgcgatga	cactgtgtat	1080
tacgatttg	caaagtgtc	taaagagcgt	cgcgaagggtt	atgcgtggta	ctccactgac	1140
ccgaataaga	cgctaaaaaa	atatgctgaa	tggctaaaaa	aatatcccaa	ataaa	1194

<210> 26

<211> 397

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(15)

<221> DOMAIN

<222> (16)...(397)

<223> Catalytic domain

<400> 26

Met	Val	Ala	Ala	Leu	Leu	Ser	Cys	Gly	Ser	Ala	Asn	Leu	Tyr	Ala	Glu
1				5					10				15		
Ser	Thr	Ala	Lys	Ser	Val	Thr	Gln	Ser	Ala	Ala	Thr	Asn	Gln	Leu	Gln
			20					25				30			
Asn	Glu	Lys	Ser	Ser	Trp	Asp	Ser	Tyr	Tyr	Ala	Ala	Ser	Lys	Lys	Ile
	35					40				45					
His	Gln	Ala	Asp	Gln	Asp	Phe	Leu	Ala	Ala	Glu	Leu	Lys	Lys	Leu	Gly
	50					55			60						
Gln	Lys	Lys	Pro	Thr	Leu	Pro	Ala	His	Thr	Lys	Asp	Phe	Gly	Phe	Asp
	65				70				75			80			
Val	Lys	Gln	Val	Asn	Ala	Asp	Trp	Phe	Lys	Ser	Asp	Glu	Gly	Lys	Arg
			85					90				95			
Val	Met	Glu	Ile	Ile	Leu	Ser	Phe	Gln	Thr	Pro	Ser	Gly	Gly	Trp	Ser
			100					105			110				
Lys	Arg	Thr	Asp	Met	Ala	Lys	Ala	Val	Arg	Gln	Pro	Gly	Gln	Ala	Phe
			115					120			125				

Gly	Val	Glu	Lys	Gly	Tyr	Ile	Pro	Thr	Phe	Asp	Asn	Gly	Ala	Thr	Ser
130				135					140						
Thr	Gln	Leu	Met	Leu	Leu	Ala	Gln	Ala	His	Gln	Ala	Thr	Gly	Asp	His
145				150					155						160
Arg	Phe	Ser	Asp	Ala	Phe	Gly	Arg	Gly	Leu	Gln	Leu	Ile	Leu	Thr	Ala
				165					170						175
Gln	Tyr	Pro	Asn	Gly	Gly	Trp	Pro	Gln	Asn	Phe	Pro	Leu	Thr	Gly	Ser
				180					185						190
Tyr	His	Asp	Tyr	Ile	Thr	Tyr	Asn	Asp	Asn	Leu	Thr	Arg	Asp	Leu	Met
				195					200						205
Val	Val	Leu	His	Lys	Thr	Ala	Gln	Ala	Lys	Asn	Asp	Phe	Ala	Phe	Val
				210					215						220
Thr	Lys	Ala	Gln	Gln	Ile	Ala	Ala	Ser	Ala	Ser	Leu	Ala	Arg	Ala	Leu
				225					230						240
Asp	Cys	Val	Leu	Lys	Ser	Gln	Val	Val	Val	Asn	Gly	Thr	Arg	Thr	Leu
				245					250						255
Trp	Gly	Ala	Gln	His	Asp	Val	Lys	Thr	Leu	Gln	Pro	Thr	Lys	Ala	Arg
				260					265						270
Ala	Phe	Glu	Met	Val	Ser	Leu	Thr	Thr	Thr	Glu	Ser	Ala	Ala	Met	Leu
				275					280						285
Ser	Phe	Leu	Met	Asp	Ile	Lys	Asn	Pro	Ser	Ala	Asp	Ile	Ile	Gln	Ser
				290					295						300
Ile	His	Ala	Ala	Ile	Ala	Trp	Tyr	Glu	Gln	Asn	Lys	Ile	Val	Gly	Lys
				305					310						320
Thr	Trp	Thr	Arg	Gly	Asp	Ala	Glu	Leu	Lys	Asp	Asn	Lys	Ser	Gln	
				325					330						335
Pro	Leu	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Lys	Pro	Ile	Phe
				340					345						350
Gly	Asp	Arg	Asp	Asp	Thr	Val	Tyr	Tyr	Asp	Leu	Ala	Lys	Val	Ser	Lys
				355					360						365
Glu	Arg	Arg	Glu	Gly	Tyr	Ala	Trp	Tyr	Ser	Thr	Asp	Pro	Asn	Lys	Thr
				370					375						380
Leu	Lys	Lys	Tyr	Ala	Glu	Trp	Ser	Lys	Lys	Tyr	Pro	Lys			
				385					390						395

<210> 27

<211> 1917

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 27

gtgtctctct	ttagaaaact	cgcaactgccg	gttctgtcg	gtctactgct	ttctgtcgga		60
gcagaaaacc	gagcgtcgaa	gcbcattgtc	gtggccgctg	atggatcg	tgacgtcagg		120
acgattcaac	aaggcgtgga	ccaggttccc	aaagacaata	cacaccggt	cttgattcag		180
atcaagccgg	gtgtgtatca	ggaacaagt	cgtgtcgccg	ccggcaaacg	ctttatcact		240
cttcgcggcg	acgacgcgag	caagaccgtc	atcacctatc	gattgagcgc	actacaagcg		300
ggaaaatacc	ggtgtgcatt	caccaccta	attaatgcag	acgactttcg	cgccgagaac		360
ctgacgtttt	aaaactcctt	ccgcaccgg	tcacaagcg	ttgctttgtt	tgtcgatgcg		420
aaccgcgcga	cgtttaaaaa	ctgcccgttc	ctcgggtggc	aggacactt	gtttgtgaac		480
ggcagccgccc	acttcttcaa	agactgctac	gtcgaaggcc	atgtcgattt	cattttcg		540
acggcctccg	cagtgtttga	gaactgcacc	attcacagca	aaggcgaagg	ttatgtgacc		600
gcbcactatc	gcaccagcg	tgagatggat	accgggtttt	tctttcatcg	ttgtcg		660
acccggacgag	acacggcccg	cggagttat	ctcggaaaggc	cgtggcgacc	ttacgcgcgc		720
gtcgtcttta	tcgattgt	gttggacgca	cacatcagac	ctgaaggctg	ggataattgg		780
agagatcctg	aacgagagaa	gaccgcgtgg	tttgccgagt	acaagtcaa	agggcccggt		840
gctaatcccg	tagctcgtgt	cgcgtgg	aggcagttga	cgacagaaca	agccgcccgg		900

ttttcgcccc	aacgctttt	cagccgcgt	gttcgcggc	tctctggca	ggccaaccag	960
gcagtccgaa	cgatcgctg	ggacgatgcg	cagaaaaaac	cgaacgagg	gtatgcagc	1020
gccgaggcgt	tgcgcacatgc	cgacaacgtt	gttcttatac	aacgtgactc	cgccggctgg	1080
cccaagaaca	tcgacatggg	gaagccgctc	gacgacaagg	gtcgagccgg	tcttctgcgc	1140
gtgcgttaaga	agaacgattc	caccatcgat	aacggcgca	cttacacgc	actctcg	1200
ctagcgccgg	tttacacggc	gcaaaaagca	gagcggc	atcgcgtt	tctgaaggga	1260
ctcgattacc	tgttgaaggc	gcagtatcca	aacggagg	gccccg	ctatccaa	1320
ctcaacggct	attacaaaca	catcactt	aacgacaacg	cgatgatcg	cgtgatgaaa	1380
ctgctgcgcg	acgtacgcgc	agcgaaaccc	gcgtatgcgt	ttgtcga	agcacgacga	1440
acgagtgcgg	cgaaggcggt	cgaaaaagga	atcgagtgc	tactgaagac	gcaggtgg	1500
gtgaatggcc	ggcgcaccgt	gtggtgtgc	caacatgac	aagtacacgt	cgcgcctg	1560
ccggcgagga	cgttgaatt	agttcgc	agtgggtg	aaagcg	gatcg	1620
ttttgtatgt	cgtcaagaa	cccg	gcgttgc	aggcgat	gtcg	1680
gcgtgg	agcaatcg	agtaaagat	cccg	ccgc	gattt	1740
tatgagatcg	gcaactatcg	tccgat	gccccg	acggcgt	taagtatgat	1800
gtgaaacaga	tcgatgagga	acgacgaa	aattacg	gtacgtt	cgacgc	1860
aaactactga	agaccgacta	tcctg	agtgg	aaagaaa	acgcca	1917
					aga	

<210> 28
<211> 638
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<221> DOMAIN
<222> (28)...(308)
<223> Pectin methyl esterase domain

<221> DOMAIN
<222> (309)...(638)
<223> Catalytic domain

<400> 28
Met Ser Leu Phe Arg Lys Leu Ala Leu Pro Val Leu Cys Gly Leu Leu
1 5 10 15
Leu Ser Val Gly Ala Glu Thr Arg Ala Ser Lys Arg Ile Val Val Ala
20 25 30
Ala Asp Gly Ser Gly Asp Val Arg Thr Ile Gln Gln Ala Val Asp Gln
35 40 45
Val Pro Lys Asp Asn Thr His Pro Val Leu Ile Gln Ile Lys Pro Gly
50 55 60
Val Tyr Gln Glu Gln Val Arg Val Ala Ala Gly Lys Arg Phe Ile Thr
65 70 75 80
Leu Arg Gly Asp Asp Ala Ser Lys Thr Val Ile Thr Tyr Arg Leu Ser
85 90 95
Ala Leu Gln Ala Gly Asn Thr Arg Leu Ala Phe Thr Thr Leu Ile Asn
100 105 110
Ala Asp Asp Phe Arg Ala Glu Asn Leu Thr Phe Glu Asn Ser Phe Gly
115 120 125
Thr Gly Ser Gln Ala Val Ala Leu Phe Val Asp Ala Asn Arg Ala Thr
130 135 140
Phe Glu Asn Cys Arg Phe Leu Gly Trp Gln Asp Thr Leu Phe Val Asn
145 150 155 160
Gly Ser Arg His Phe Phe Lys Asp Cys Tyr Val Glu Gly His Val Asp

165	170	175
Phe Ile Phe Gly Thr Ala Ser Ala Val Phe	Glu Asn Cys Thr Ile His	
180	185	190
Ser Lys Gly Glu Gly Tyr Val Thr Ala His	Tyr Arg Thr Ser Asp Glu	
195	200	205
Met Asp Thr Gly Phe Val Phe His Arg Cys	Arg Leu Thr Gly Arg Asp	
210	215	220
Thr Gly Arg Gly Val Tyr Leu Gly Arg Pro	Trp Arg Pro Tyr Ala Arg	
225	230	240
Val Val Phe Ile Asp Cys Trp Leu Asp Ala	His Ile Arg Pro Glu Gly	
245	250	255
Trp Asp Asn Trp Arg Asp Pro Glu Arg Glu	Lys Thr Ala Trp Phe Ala	
260	265	270
Glu Tyr Lys Ser Lys Gly Pro Gly Ala Asn	Pro Val Ala Arg Val Ala	
275	280	285
Trp Ser Arg Gln Leu Thr Thr Glu Gln Ala	Ala Glu Phe Ser Arg Glu	
290	295	300
Arg Phe Phe Ser Arg Ala Val Arg Gly Leu	Ser Gly Gln Ala Asn Gln	
305	310	320
Ala Val Gly Thr Ile Ala Trp Asp Asp Ala	Gln Lys Lys Pro Asn Glu	
325	330	335
Trp Tyr Ala Ser Ala Glu Ala Leu Arg Ile	Ala Asp Asn Val Val Leu	
340	345	350
Tyr Gln Arg Asp Ser Gly Gly Trp Pro Lys	Asn Ile Asp Met Gly Lys	
355	360	365
Pro Leu Asp Asp Lys Gly Arg Ala Gly Leu	Leu Arg Val Arg Lys Lys	
370	375	380
Asn Asp Ser Thr Ile Asp Asn Gly Ala Thr	Tyr Thr Gln Leu Ser Phe	
385	390	400
Leu Ala Arg Val Tyr Thr Ala Gln Lys Gln	Glu Arg His Arg Glu Ser	
405	410	415
Phe Leu Lys Gly Leu Asp Tyr Leu Leu Lys	Ala Gln Tyr Pro Asn Gly	
420	425	430
Gly Trp Pro Gln Phe Tyr Pro Asn Leu Asn	Gly Tyr Tyr Lys His Ile	
435	440	445
Thr Phe Asn Asp Asn Ala Met Ile Gly Val	Met Lys Leu Leu Arg Asp	
450	455	460
Val Ala Ala Ala Lys Pro Ala Tyr Ala Phe	Val Asp Glu Ala Arg Arg	
465	470	480
Thr Ser Ala Ala Lys Ala Val Glu Lys Gly	Ile Glu Cys Ile Leu Lys	
485	490	495
Thr Gln Val Val Val Asn Gly Arg Arg	Thr Val Trp Cys Ala Gln His	
500	505	510
Asp Glu Val Thr Leu Ala Pro Ala Arg Thr	Phe Glu Leu Val	
515	520	525
Ser Leu Ser Gly Gly Glu Ser Val Glu Ile	Val Arg Phe Leu Met Ser	
530	535	540
Ile Lys Asn Pro Ser Pro Ala Val Val Glu	Ala Ile Glu Ser Ala Val	
545	550	560
Ala Trp Phe Glu Gln Ser Gln Val Lys Asp	Pro Ala Gly Lys Pro Ala	
565	570	575
Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn	Arg Pro Ile Phe Ala Gly	
580	585	590
Arg Asp Gly Val Val Lys Tyr Asp Val Lys	Gln Ile Asp Glu Glu Arg	
595	600	605
Arg Lys Asn Tyr Ala Trp Tyr Val Asp Asp	Ala Ala Lys Leu Leu Lys	
610	615	620
Thr Asp Tyr Pro Glu Trp Lys Glu Lys Asn	Ala Lys Asp Gln	
625	630	635

Pro Con Var Lys Deu / Ser Ile Ele Thr Ser

<210> 29
<211> 1398
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 29

atgattaacc	gtcgagattt	cataaaagac	ctcatcatca	cctccgccgg	agtgcgggtt	60
ctcccgcaac	tggcggtcgg	acaaaacgt	ccctggaaaa	ctcaatacc	gcagatcc	120
gcgcggatca	aaccggcga	atttccgaag	cgcgatttcg	tcatcacgaa	gttcggcg	180
aaggcgggaa	ccgatagcac	gcaagcgatc	gctaaagccc	tcgacgctt	cgcgaaagcc	240
ggcggcggac	gcgtcgctgt	acccggccgg	gaatttctca	ccggtgcgat	ccatctcaag	300
tcaaacacca	atctctacgt	ctcaaaaggc	gchgactctga	agttttcgac	cgaccccgaa	360
aaatatctgc	cgatcgttca	cacgcggtgtt	gaaggatgg	agtttgatgca	tctctcgccg	420
ttcatctacg	cgtacgagca	gacgaacatc	gcatcacc	gcgagggcac	gctcgacggc	480
caaggcaat	cgttctttt	gaagtggcac	ggcaacccgc	gatacggcgg	caaccccgaa	540
gtgatcagtc	agcaaaaagc	gcgggcgcga	ctttacgaga	tgtatggacaa	gaacgtaccc	600
gtcgccggac	gcgtgttcgg	tatcgccgcac	tatctccggc	cgcagttcat	ccagccgtac	660
aaatgtttaa	acgtcttgc	cgaaggcggt	acgatcatcg	actcgccat	gtgggaagtt	720
catccgggtc	tttgcgagaa	tgtcaccgtc	cgcaatcttc	acatctcg	gcacggtccg	780
aacaacgacg	gctgcgatcc	cgagtcgtgc	aaagacgtcc	tgtatcgacaa	ctgcttcttc	840
gacaccgggt	acgactgcat	cgcgatcaag	tcgggtcgca	ataacgacgg	tcgtcgtctg	900
aacacaccga	ccgagaacat	catcgccgc	aactgcacga	tggaaagacgg	tcacgggtgg	960
atcacgggtc	gaagcgagat	ctcgccggc	gtgcgaaact	tgttcgcaca	cgattgcaag	1020
atggacagt	cggatctgt	gaccgcgtc	cgggtaaaga	acaacgcac	gcggggcggc	1080
atgctggaga	atttctattt	ccgcaacatc	accgtcgccg	aagtcgcgcg	tgctgtggtc	1140
gagatcgatt	tcaactatga	agaaggcg	aaggatcg	acacaccgt	catgcgcaac	1200
tacgtggtc	aggatctgac	gtgcacc	ggaaaccggc	ccgtcgatct	gcaaggatta	1260
gacaacgcgc	caatttacga	tgtgtcgct	cgttaacacga	ccttcggcgc	gatgaagaac	1320
aagagcgtcg	tgaagaatgt	ccgaggactg	aagatcgaaa	acgttaccgt	cagcggcacg	1380
cgcggtggaga	gtttatga					1398

<210> 30
<211> 465
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(27)

<221> DOMAIN
<222> (77)...(459)
<223> Catalytic domain

<400> 30

Met	Ile	Asn	Arg	Arg	Asp	Phe	Ile	Lys	Asp	Leu	Ile	Ile	Thr	Ser	Ala
1						5				10					15
Gly	Val	Ala	Val	Leu	Pro	Gln	Leu	Ala	Phe	Gly	Gln	Asn	Asp	Pro	Trp
										20	25				30
Lys	Thr	Gln	Tyr	Pro	Gln	Ile	Leu	Ala	Arg	Ile	Lys	Pro	Pro	Lys	Phe
										35	40				45
Pro	Lys	Arg	Asp	Phe	Val	Ile	Thr	Lys	Phe	Gly	Ala	Lys	Ala	Gly	Thr
										50	55				60

Asp Ser Thr Gln Ala Ile Ala Lys Ala Leu Asp Ala Cys Ala Lys Ala
 65 70 75 80
 Gly Gly Gly Arg Val Val Val Pro Ala Gly Glu Phe Leu Thr Gly Ala
 85 90 95
 Ile His Leu Lys Ser Asn Thr Asn Leu Tyr Val Ser Lys Gly Ala Thr
 100 105 110
 Leu Lys Phe Ser Thr Asp Pro Glu Lys Tyr Leu Pro Ile Val His Thr
 115 120 125
 Arg Trp Glu Gly Met Glu Leu Met His Leu Ser Pro Phe Ile Tyr Ala
 130 135 140
 Tyr Glu Gln Thr Asn Ile Ala Ile Thr Gly Glu Gly Thr Leu Asp Gly
 145 150 155 160
 Gln Gly Lys Ser Phe Phe Trp Lys Trp His Gly Asn Pro Arg Tyr Gly
 165 170 175
 Gly Asn Pro Glu Val Ile Ser Gln Gln Lys Ala Arg Ala Arg Leu Tyr
 180 185 190
 Glu Met Met Asp Lys Asn Val Pro Val Ala Glu Arg Val Phe Gly Ile
 195 200 205
 Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro Tyr Lys Cys Lys Asn
 210 215 220
 Val Leu Ile Glu Gly Val Thr Ile Ile Asp Ser Pro Met Trp Glu Val
 225 230 235 240
 His Pro Val Leu Cys Glu Asn Val Thr Val Arg Asn Leu His Ile Ser
 245 250 255
 Ser His Gly Pro Asn Asn Asp Gly Cys Asp Pro Glu Ser Cys Lys Asp
 260 265 270
 Val Leu Ile Asp Asn Cys Phe Phe Asp Thr Gly Asp Asp Cys Ile Ala
 275 280 285
 Ile Lys Ser Gly Arg Asn Asn Asp Gly Arg Arg Leu Asn Thr Pro Thr
 290 295 300
 Glu Asn Ile Ile Val Arg Asn Cys Thr Met Lys Asp Gly His Gly Gly
 305 310 315 320
 Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val Arg Asn Leu Phe Ala
 325 330 335
 His Asp Cys Lys Met Asp Ser Ala Asp Leu Trp Thr Ala Leu Arg Val
 340 345 350
 Lys Asn Asn Ala Ser Arg Gly Gly Met Leu Glu Asn Phe Tyr Phe Arg
 355 360 365
 Asn Ile Thr Val Gly Gln Val Ala Arg Ala Val Val Glu Ile Asp Phe
 370 375 380
 Asn Tyr Glu Glu Gly Ala Lys Gly Ser Tyr Thr Pro Val Met Arg Asn
 385 390 395 400
 Tyr Val Val Glu Asp Leu Thr Cys Thr Ser Gly Asn Arg Pro Val Asp
 405 410 415
 Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asp Val Ser Leu Arg Asn
 420 425 430
 Thr Thr Phe Gly Ala Met Lys Asn Lys Ser Val Val Lys Asn Val Arg
 435 440 445
 Gly Leu Lys Ile Glu Asn Val Thr Val Ser Gly Thr Arg Val Glu Ser
 450 455 460

Leu
 465

<210> 31
 <211> 1401
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 31

atgatcaatc	tttatggcgt	cttgacatc	cggaccttg	ggcccaacc	ggacggagaa	60
acgccttcca	ctgcggcgat	tacggcggcc	atcgaaaactt	gtgccgcggc	cgggggagga	120
gtggcttaca	tcccggccgg	acggttccctc	accggcccc	tccgcctcaa	aagccacgtc	180
cggctccatc	tcgagggccgg	agcgcacttg	ctcttttagtc	aggacccggc	cgattatcct	240
gttctggaga	cgaggtggga	ggggaaaggag	gtcttgcacct	atgcacaccca	gatctacggc	300
gaggacctcg	aagggttcgc	gattaccgg	cgggggacca	tcgacggccg	gggcgagact	360
tgtggcgac	tcttcgcgc	caaagccttc	acccatcccc	gacccgcct	catgccttt	420
accgcgtca	aggacatcct	gatagaagga	gtaaccctcg	tcaattcacc	ggcctggacc	480
atcaatcctg	tgtatgtcga	gcgggtgacc	atcgataagg	tgactatcat	caaccggccc	540
gactcgccca	acaccgacgg	gatcgacccc	gattcctccc	ggaacgtcta	tatcactaac	600
tgtctacattg	acgttaggcga	tgactgcattc	gccatcaaag	cgggccgaga	ggactccctt	660
tatcgacgc	cttggaaaa	cattgtcattc	gccaactgccc	tcatgcgc	cggtcacggc	720
gggggtgtca	tcggcagcga	gaccagcggg	ggtattcgca	aggtatgtcat	taccaactgc	780
atcttcgagg	acaccgacgg	gggcattttaga	cttaagtccc	ggcgcggacg	cggcgggttc	840
gtcgaggacc	tccggcgcac	aatattttatc	atggaaaagg	tgctctgtcc	cttcgtcctc	900
aacatgtact	atgataccgg	gggaggcgtg	atcgacgagc	gcccgcatga	cttagaacccc	960
catccggtaa	gcgaggctac	accctccttc	cgccgcctct	cttcagtc	cattactgccc	1020
cggaaagtgc	aggccgcgc	ggccttcctc	tacggcctgc	ccgaacagcc	tctggaggac	1080
gtcttatttg	acgatatatctg	gatagagctg	gccgcgcacg	cttctctgc	cggtccggcc	1140
atgatgcggg	ccgtcccgcc	catgagccaa	ggtgtgtgc	tctgtctacgg	tgccgcggcgg	1200
atctccttcc	ggcacatgca	cctccgcggg	caccgcggc	ccgccttcca	gatcgaacgc	1260
gcccggcgg	tgcagttgt	gggctgctcg	accgacggca	gtgaagaccc	ccagcttgcc	1320
ttgggtcaag	cgaggaggt	caccatccgt	gactgcaccc	ttaccgc	gcaggacccc	1380
gcaaaagaaa	ggcaaaat	a				1401

<210> 32

<211> 466

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(348)

<223> Catalytic domain

<400> 32

Met	Ile	Asn	Leu	Tyr	Gly	Val	Phe	Asp	Ile	Arg	Thr	Phe	Gly	Ala	Gln
1				5				10					15		
Pro	Asp	Gly	Glu	Thr	Pro	Ser	Thr	Ala	Ala	Ile	Thr	Ala	Ala	Ile	Glu
				20				25					30		
Thr	Cys	Ala	Ala	Ala	Gly	Gly	Val	Val	Tyr	Ile	Pro	Ala	Gly	Arg	
				35				40					45		
Phe	Leu	Thr	Gly	Pro	Leu	Arg	Leu	Lys	Ser	His	Val	Arg	Leu	His	Leu
	50				55				60						
Glu	Ala	Gly	Ala	His	Leu	Leu	Phe	Ser	Gln	Asp	Pro	Ala	Asp	Tyr	Pro
65					70				75					80	
Val	Leu	Glu	Thr	Arg	Trp	Glu	Gly	Lys	Glu	Val	Leu	Thr	Tyr	Ala	His
				85				90					95		
Gln	Ile	Tyr	Gly	Glu	Asp	Leu	Glu	Gly	Val	Ala	Ile	Thr	Gly	Arg	Gly
	100				105				110						
Thr	Ile	Asp	Gly	Arg	Gly	Glu	Thr	Trp	Trp	Arg	Leu	Phe	Arg	Ala	Lys
	115				120						125				
Ala	Phe	Thr	His	Pro	Arg	Pro	Arg	Leu	Ile	Ala	Phe	Thr	Arg	Cys	Lys
	130				135				140						

Asp Ile Leu Ile Glu Gly Val Thr Leu Val Asn Ser Pro Ala Trp Thr
 145 150 155 160
 Ile Asn Pro Val Met Cys Glu Arg Val Thr Ile Asp Lys Val Thr Ile
 165 170 175
 Ile Asn Pro Pro Asp Ser Pro Asn Thr Asp Gly Ile Asp Pro Asp Ser
 180 185 190
 Ser Arg Asn Val Tyr Ile Thr Asn Cys Tyr Ile Asp Val Gly Asp Asp
 195 200 205
 Cys Ile Ala Ile Lys Ala Gly Arg Glu Asp Ser Leu Tyr Arg Thr Pro
 210 215 220
 Cys Glu Asn Ile Val Ile Ala Asn Cys Leu Met Arg His Gly His Gly
 225 230 235 240
 Gly Val Val Ile Gly Ser Glu Thr Ser Gly Gly Ile Arg Lys Val Val
 245 250 255
 Ile Thr Asn Cys Ile Phe Glu Asp Thr Asp Arg Gly Ile Arg Leu Lys
 260 265 270
 Ser Arg Arg Gly Arg Gly Phe Val Glu Asp Leu Arg Ala Thr Asn
 275 280 285
 Ile Ile Met Glu Lys Val Leu Cys Pro Phe Val Leu Asn Met Tyr Tyr
 290 295 300
 Asp Thr Gly Gly Val Ile Asp Glu Arg Ala His Asp Leu Glu Pro
 305 310 315 320
 His Pro Val Ser Glu Ala Thr Pro Ser Phe Arg Arg Leu Ser Phe Ser
 325 330 335
 His Ile Thr Ala Arg Glu Val Gln Ala Ala Ala Ala Phe Leu Tyr Gly
 340 345 350
 Leu Pro Glu Gln Pro Leu Glu Asp Val Leu Phe Asp Asp Ile Trp Ile
 355 360 365
 Glu Leu Ala Ala Asp Ala Ser Pro Ala Arg Pro Ala Met Met Arg Ala
 370 375 380
 Val Pro Pro Met Ser Gln Gly Gly Val Leu Cys Tyr Gly Ala Arg Arg
 385 390 395 400
 Ile Ser Phe Arg His Met His Leu Arg Gly His Arg Gly Pro Ala Phe
 405 410 415
 Gln Ile Glu Arg Ala Glu Ala Val Gln Leu Met Gly Cys Ser Thr Asp
 420 425 430
 Gly Ser Glu Asp Pro Gln Leu Val Leu Gly Gln Ala Glu Glu Val Thr
 435 440 445
 Ile Arg Asp Cys Thr Phe Thr Ala Gln Gln Asp Pro Ala Lys Glu Arg
 450 455 460
 Gln Asn
 465

<210> 33
 <211> 1041
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 33
 atgaaaacttc gatgtctgat gctcaccctg cttctttgcg gcagcgccctt cgccggccgac 60
 cggattacgg ccgacaagat caacaacaag cccgactcct ggcttaccag cgacgaaggc 120
 atcaagctga tcgacaacat catcacctgg cagaaccccg agggtggctg ggccaagtac 180
 tacgacgcga ccaatccgca caaacaaggc gaagtctacg gcgactggga cggcgctcggc 240
 accatcgaca acggctacac ctacaccgag ctgaatctcc tggcgcacgt ctacaccctc 300
 accaagcgcc cggagatcct cgattcgttc aacaagggcc tggagttct gctcaaagcc 360
 caatacccca gcgccgctg gcccacacgg tttccgggtgc ccaacaacta cggcaagtgc 420

atcacgctca	acgacaacgc	gatggtaaac	gtgatgcagt	tcctgcagaa	cgtcgcaaag	480
ggcaaggaag	acttcgctt	cgtcgacgag	cagcgtcgcg	ccaaagcga	ggagggcg	540
gaccgcggga	tcgactgcct	tctgaagctc	cagattaccg	tgaacggca	gcttaccgc	600
tggggccagc	agtatgaccc	gaagacactc	gccgcggcgc	ccgcccggc	gtacgagctc	660
ccgggcctca	gcggctgcga	aagcgcgc	gtcatgcgt	tgttcatgtc	tttggagaac	720
cccagtcccc	aagttcagcg	cgccgtccac	gcggcggcg	cttggtaacg	ggcgtcgaag	780
atcaccggca	agaagctggt	gchgagaaac	aacgacgtga	cactggccga	cgacccaaac	840
ggcgagccgc	tttgggcgc	tttctacgac	atcgaaaacca	accgccc	tttgcgt	900
cgcgacggcg	tgaagaagt	gtcgctggac	gagatcgagc	ccgaacggc	caagggctac	960
gcttgggtcc	gcccctggc	gacgagcgt	ctggagcgt	atcgcaagt	ggcggcgaag	1020
caccaccc	tgaacagtt	a				1041

<210> 34

<211> 346

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(18)

<221> DOMAIN

<222> (19)...(346)

<223> Catalytic domain

<400> 34

Met	Lys	Leu	Arg	Cys	Leu	Met	Leu	Thr	Leu	Leu	Leu	Cys	Gly	Ser	Ala
1						5			10						15
Phe	Ala	Ala	Asp	Arg	Ile	Thr	Ala	Asp	Lys	Ile	Asn	Asn	Lys	Pro	Asp
						20			25						30
Ser	Trp	Leu	Thr	Ser	Asp	Glu	Gly	Ile	Lys	Leu	Ile	Asp	Asn	Ile	Ile
						35			40						45
Thr	Trp	Gln	Asn	Pro	Glu	Gly	Gly	Trp	Ala	Lys	Tyr	Tyr	Asp	Ala	Thr
						50			55						60
Asn	Pro	His	Lys	Gln	Gly	Glu	Val	Tyr	Gly	Asp	Trp	Asp	Gly	Val	Gly
						65			70						80
Thr	Ile	Asp	Asn	Gly	Tyr	Thr	Tyr	Thr	Glu	Leu	Asn	Leu	Leu	Ala	His
						85			90						95
Val	Tyr	Thr	Leu	Thr	Lys	Arg	Pro	Glu	Ile	Leu	Asp	Ser	Phe	Asn	Lys
						100			105						110
Gly	Leu	Glu	Phe	Leu	Leu	Lys	Ala	Gln	Tyr	Pro	Ser	Gly	Gly	Trp	Pro
						115			120						125
Gln	Arg	Phe	Pro	Val	Pro	Asn	Asn	Tyr	Gly	Lys	Cys	Ile	Thr	Leu	Asn
						130			135						140
Asp	Asn	Ala	Met	Val	Asn	Val	Met	Gln	Phe	Leu	Gln	Asn	Val	Ala	Lys
							145		150						160
Gly	Lys	Glu	Asp	Phe	Ala	Phe	Val	Asp	Glu	Gln	Arg	Arg	Ala	Lys	Ala
							165		170						175
Lys	Glu	Ala	Phe	Asp	Arg	Gly	Ile	Asp	Cys	Leu	Leu	Lys	Leu	Gln	Ile
							180		185						190
Thr	Val	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Ala	Gln	Gln	Tyr	Asp	Pro	Lys
							195		200						205
Thr	Leu	Ala	Ala	Ala	Pro	Ala	Arg	Ala	Tyr	Glu	Leu	Pro	Gly	Leu	Ser
							210		215						220
Gly	Cys	Glu	Ser	Ala	Pro	Val	Met	Arg	Leu	Phe	Met	Ser	Leu	Glu	Asn
							225		230						240
Pro	Ser	Pro	Glu	Val	Gln	Arg	Ala	Val	His	Ala	Ala	Ala	Trp	Tyr	

	245	250	255												
Glu	Ala	Ser	Lys	Ile	Thr	Gly	Lys	Lys	Leu	Val	Arg	Glu	Asn	Asn	Asp
	260						265					270			
Val	Thr	Leu	Ala	Asp	Asp	Pro	Asn	Gly	Glu	Pro	Leu	Trp	Ala	Arg	Phe
	275						280					285			
Tyr	Asp	Ile	Glu	Thr	Asn	Arg	Pro	Phe	Tyr	Cys	Gly	Arg	Asp	Gly	Val
	290					295				300					
Lys	Lys	Trp	Ser	Leu	Asp	Glu	Ile	Glu	Pro	Glu	Arg	Arg	Lys	Gly	Tyr
	305				310				315				320		
Ala	Trp	Val	Arg	Pro	Trp	Ala	Thr	Ser	Val	Leu	Glu	Gln	Tyr	Arg	Lys
							325		330				335		
Trp	Ala	Ala	Lys	His	Pro	Pro	Val	Asn	Ser						
							340		345						

<210> 35

<211> 1071

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 35

atgccaaaaa	attccgacgaa	cgcgtggcgg	aaaaagactc	cgcggatttgc	gagtcttgc	60
acatggaggc	acgttattcaa	acagaaggct	ctctggtacc	aaaccgacgaa	ggcggtcgaa	120
gtcgccggacc	aactcctcat	ctatcaaaaaa	gagaacggcg	gttttgagaa	aatgtcgac	180
atggcgttga	tgctgacgca	gaaggaaaaaa	gaagagctca	ccgcaaagcg	gtcagacgtc	240
tccgaaacgaa	cgtatcgacaa	ccggaccacg	tatcctcagg	tgcgtatct	cggtcgagta	300
atcaccgcaa	gccttcttaa	acattcgccg	ccggcgaatc	ttccgaaata	caaagacgccc	360
ttcaacaaag	gtcttgatta	cctgcttgcc	tcccagtatg	agaacggagg	atttccgca	420
ttctatccgt	tgaaaaaaagg	ctattacaca	cacatcacct	tcaacgacga	cgcgtatgatc	480
ggcgtcctga	aggtgcttcg	cgacatcgca	aataaaaaag	aggattacgt	gttcgtggat	540
gaagcgcgaa	gacttcgcgc	cgagcaagcg	gtcgccaaag	cgctgcctt	tattctgaag	600
cttcagggtt	tcgtcgacgg	aaagaaaaacc	gtctggctg	cgcgtatgaa	cgagactacg	660
ctggcgctcg	cagcggctcg	caagttttag	cccggtctgt	tgaccgctgg	tgagagcg	720
ggcatcgatcc	gataacctgat	gcaggaaaaaa	ccgaccccg	agatcacccg	tgcgtatcgag	780
tctgcgtatcg	attggatcg	aaagaacaag	atcgacggaa	tacgttggaa	gcatcgatccaa	840
ggcgagaaca	cggttgtgaa	agacaaatcg	gtccccctaa	tatgggcacg	gttctatcgag	900
atcgaaacgaa	tgcgtccgat	cttcatcgga	cgtgattcgg	ttatcaagta	tgacgtgacg	960
caggtcgaag	ccgagcgtcg	aatggttac	gcctgtacg	tcacccgcacc	aatgtaaattg	1020
gtgaacgagg	attatttggaa	gttggaaagggg	aaaagcgccg	gagccaaagta	g	1071

<210> 36

<211> 356

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(356)

<223> Catalytic domain

<400> 36

Met	Pro	Lys	Asn	Ser	Asp	Asp	Ala	Trp	Arg	Glu	Lys	Thr	Pro	Pro	Asp
1				5					10				15		
Trp	Ser	Leu	Val	Thr	Trp	Ser	Asp	Val	Phe	Lys	Gln	Lys	Pro	Leu	Trp
								20		25			30		

Tyr Gln Thr Asp Glu Ala Ala Arg Val Ala Asp Gln Leu Leu Ile Tyr
 35 40 45
 Gln Lys Glu Asn Gly Gly Phe Glu Lys Asn Val Asp Met Ala Leu Met
 50 55 60
 Leu Thr Gln Lys Glu Lys Glu Leu Thr Ala Lys Arg Ser Asp Val
 65 70 75 80
 Ser Glu Thr Thr Ile Asp Asn Arg Thr Thr Tyr Pro Gln Val Ala Tyr
 85 90 95
 Leu Gly Arg Val Ile Thr Ala Ser Leu Leu Lys Pro Ser Pro Pro Ala
 100 105 110
 Asn Leu Pro Lys Tyr Lys Asp Ala Phe Asn Lys Gly Leu Asp Tyr Leu
 115 120 125
 Leu Ala Ser Gln Tyr Glu Asn Gly Gly Phe Pro Gln Phe Tyr Pro Leu
 130 135 140
 Lys Lys Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asp Ala Met Ile
 145 150 155 160
 Gly Val Leu Lys Val Leu Arg Asp Ile Ala Asn Lys Lys Glu Asp Tyr
 165 170 175
 Val Phe Val Asp Glu Ala Arg Arg Leu Arg Ala Glu Gln Ala Val Ala
 180 185 190
 Lys Ala Leu Pro Leu Ile Leu Lys Leu Gln Val Val Val Asp Gly Lys
 195 200 205
 Lys Thr Val Trp Ala Ala Gln Tyr Asp Glu Thr Thr Leu Ala Pro Ala
 210 215 220
 Ala Ala Arg Lys Phe Glu Pro Val Ser Leu Thr Ala Gly Glu Ser Val
 225 230 235 240
 Gly Ile Val Arg Tyr Leu Met Gln Glu Lys Pro Thr Pro Glu Ile Thr
 245 250 255
 Asp Ala Ile Glu Ser Ala Ile Asp Trp Tyr Arg Lys Asn Lys Ile Asp
 260 265 270
 Gly Ile Arg Trp Glu Arg Ile Lys Gly Glu Asn Thr Val Val Lys Asp
 275 280 285
 Lys Ser Ala Pro Pro Ile Trp Ala Arg Phe Tyr Gln Ile Glu Thr Met
 290 295 300
 Arg Pro Ile Phe Ile Gly Arg Asp Ser Val Ile Lys Tyr Asp Val Thr
 305 310 315 320
 Gln Val Glu Ala Glu Arg Arg Asn Gly Tyr Ala Trp Tyr Val Thr Ala
 325 330 335
 Pro Asn Glu Leu Val Asn Glu Asp Tyr Leu Lys Trp Lys Gly Lys Ser
 340 345 350
 Ala Gly Ala Lys
 355

<210> 37

<211> 1860

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 37

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atagcagccg ctgttgcgtt gatggcaggc	acttcagcat ttgcagctgc gacgggtggc	120
ttctctacca ctgatggtgg caacgtatcg	ggcgcgggtt cgtttactgc atcgacttac	180
cagcaaatca acaccattat tgccaacgc	aaactggatg atgcaggtaa aaaagtca	240
gggggtgctt acccgcttat cattacctac	accggtaatg aagactcgct gattaaccag	300
atgatcaaag accacacgg	gaattcatcg ggcaactgcc ctaaccgcg	360
gcctatcgct acgtggaaat taaaagat	ttaccattca accaaggta aggcgcaat	420

ggttcttcag	caaacttcgg	cattgtgatt	aataaatctg	acaatgtgat	tgtgcgtaat	480
atgaaaatcg	gtgcgcttgc	tgggatcgagt	aacgatgcgg	atatgattcg	tatcgacacc	540
ggcgtaacg	tgtggattga	tcacaacgaa	ttgttgcgg	taaataatga	atgtaaaaggt	600
tcacccgatg	gtgacctgac	atttgaaggt	gcgattgata	ttaaaaaaagc	atcgaaaaat	660
attacgggt	cctacaacat	tatccgcgt	agtaaaaaag	tagggctcga	tggttcgagt	720
agcagtgata	ttgcaggtgg	ccgtaagatt	acgttccatc	acaatattt	tcgcaatgtt	780
ggtcacggtt	taccgttgc	acgcgggtgt	tggacacaca	tgtataacaa	tcttacgac	840
ggagttacca	gctcggttat	taacgttgc	caaggtggct	acgcgcta	cgagaacaac	900
tggttccaaa	atgctgtcaa	cccggttacc	tgccgtttt	acagtagtaa	ctgcggttac	960
tggatctgc	gcaacaacaa	cgtgcgcaac	cctgggtatt	tctccaccta	caacattacc	1020
tggaccagcg	gtggcaccat	cgacgccacc	aactgacta	ccactcaacc	tttccgatt	1080
agcattcctt	acagctactc	gcctgttagc	ccgcagtgt	tcaaagacaa	gttggcaa	1140
tatgctggtg	tcggtaaaaa	caatgcgca	ttaacggcgt	ctgcgtgcag	cggaaatact	1200
tcatcggtag	cacccatc	agtgcagca	tcatccgcgg	cacccatc	ccgttcatcc	1260
agcagtgcag	cgccatccag	cacaccaact	acatcaagct	cgagttca	tgccgcaacc	1320
ggtcattt	cgctcggtgc	aacggcaacc	aacaacagca	ttgtgttag	ttggtcaccc	1380
aacaatgtga	cgctcggttc	gcaagaagt	tatcgacata	ccgacgctga	tccatcgggg	1440
cgtgtcgta	tcgcattccct	ggctgcttca	gcccgtatgt	ataccgata	cacagccgca	1500
tcggccaaa	cctattacta	ctggattaa	aataccactt	ctgggtttgt	caccaattcc	1560
aatgctgcat	cagcgcgtat	tggtagcacc	gcgtccagg	ctgttgcata	aagcagctca	1620
agttcaagcg	gcggcgcgc	cgtatttaggt	ggtaactgg	attatccaag	cggcttctcc	1680
aagtgcgtg	atttggcg	gactgttca	gtgtcatcg	gcatggctg	gttgcgtt	1740
ggtcgcaaaag	gcaagtgggt	taccaagaa	gtatcgtag	gtagttcaat	cgccgttacc	1800
ttgcggcat	ttggttcga	tccacaggc	aaccctaaca	agtgttcta	caaacgttaa	1860

<210> 38

<211> 619

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(35)

<221> DOMAIN

<222> (36)...(387)

<223> Catalytic domain

<400> 38

Met	Phe	Thr	Thr	Thr	Gly	Ser	His	Cys	Ala	Arg	Asn	Ser	Ala	Arg	Phe
1					5				10					15	
Ser	Leu	Thr	Ala	Ile	Ala	Ala	Ala	Val	Ala	Leu	Met	Ala	Gly	Thr	Ser
								20			25		30		
Ala	Phe	Ala	Ala	Ala	Ala	Thr	Gly	Gly	Phe	Ser	Thr	Thr	Asp	Gly	Asn
								35		40		45			
Val	Ser	Gly	Ala	Arg	Ser	Phe	Thr	Ala	Ser	Thr	Tyr	Gln	Gln	Ile	Asn
								50		55		60			
Thr	Ile	Ile	Ala	Asn	Ala	Lys	Leu	Asp	Asp	Ala	Gly	Lys	Lys	Val	Thr
								65		70		75		80	
Gly	Gly	Ala	Tyr	Pro	Leu	Ile	Ile	Thr	Tyr	Thr	Gly	Asn	Glu	Asp	Ser
									85		90		95		
Leu	Ile	Asn	Gln	Met	Ile	Lys	Asp	His	Thr	Val	Asn	Ser	Ser	Gly	Asn
								100		105		110			
Cys	Pro	Asn	Pro	Arg	Trp	Ser	Glu	Ala	Tyr	Arg	Tyr	Val	Glu	Ile	Lys
								115		120		125			
Glu	Phe	Thr	Lys	Gly	Ile	Thr	Ile	Gln	Gly	Ala	Asn	Gly	Ser	Ser	Ala
								130		135		140			

Asn Phe Gly Ile Val Ile Asn Lys Ser Asp Asn Val Ile Val Arg Asn
 145 150 155 160
 Met Lys Ile Gly Ala Leu Ala Gly Ala Ser Asn Asp Ala Asp Met Ile
 165 170 175
 Arg Ile Asp Thr Gly Val Asn Val Trp Ile Asp His Asn Glu Leu Phe
 180 185 190
 Ala Val Asn Asn Glu Cys Lys Gly Ser Pro Asp Gly Asp Leu Thr Phe
 195 200 205
 Glu Ser Ala Ile Asp Ile Lys Lys Ala Ser Gln Asn Ile Thr Val Ser
 210 215 220
 Tyr Asn Ile Ile Arg Asp Ser Lys Lys Val Gly Leu Asp Gly Ser Ser
 225 230 235 240
 Ser Ser Asp Ile Ala Gly Gly Arg Lys Ile Thr Phe His His Asn Ile
 245 250 255
 Tyr Arg Asn Val Gly Ala Arg Leu Pro Leu Gln Arg Gly Gly Trp Thr
 260 265 270
 His Met Tyr Asn Asn Leu Tyr Asp Gly Val Thr Ser Ser Gly Ile Asn
 275 280 285
 Val Arg Gln Gly Gly Tyr Ala Leu Ile Glu Asn Asn Trp Phe Gln Asn
 290 295 300
 Ala Val Asn Pro Val Thr Cys Arg Phe Asp Ser Ser Asn Cys Gly Tyr
 305 310 315 320
 Trp Asp Leu Arg Asn Asn Asn Val Arg Asn Pro Gly Asp Phe Ser Thr
 325 330 335
 Tyr Asn Ile Thr Trp Thr Ser Gly Gly Thr Ile Asp Ala Thr Asn Trp
 340 345 350
 Thr Thr Thr Gln Pro Phe Pro Ile Ser Ile Pro Tyr Ser Tyr Ser Pro
 355 360 365
 Val Ser Pro Gln Cys Val Lys Asp Lys Leu Ala Asn Tyr Ala Gly Val
 370 375 380
 Gly Lys Asn Asn Ala Gln Leu Thr Ala Ser Ala Cys Ser Gly Asn Thr
 385 390 395 400
 Ser Ser Val Ala Pro Ser Ser Val Pro Ala Ser Ser Ala Ala Pro Ser
 405 410 415
 Ser Arg Ser Ser Ser Ala Ala Pro Ser Ser Thr Pro Thr Thr Ser
 420 425 430
 Ser Ser Ser Val Ala Ala Thr Gly Ser Ile Ser Leu Gly Ala Thr
 435 440 445
 Ala Thr Asn Asn Ser Ile Val Leu Ser Trp Ser Pro Asn Asn Val Thr
 450 455 460
 Leu Gly Ser Gln Glu Val Tyr Arg Asp Thr Asp Ala Asp Pro Ser Gly
 465 470 475 480
 Arg Val Arg Ile Ala Ser Leu Ala Ala Ser Ala Arg Met Tyr Thr Asp
 485 490 495
 Ser Thr Ala Ala Ser Gly Gln Thr Tyr Tyr Trp Ile Lys Asn Thr
 500 505 510
 Thr Ser Gly Val Val Thr Asn Ser Asn Ala Ala Ser Ala Arg Ile Gly
 515 520 525
 Ser Thr Ala Ser Ser Ser Val Ala Ser Ser Ser Ser Ser Ser Gly
 530 535 540
 Gly Ala Pro Val Leu Gly Gly Thr Gly Asp Tyr Pro Ser Gly Phe Ser
 545 550 555 560
 Lys Cys Ala Asp Leu Gly Gly Thr Cys Ser Val Ser Ser Gly Asp Gly
 565 570 575
 Trp Val Ala Phe Gly Arg Lys Gly Lys Trp Val Thr Lys Lys Val Ser
 580 585 590
 Val Gly Ser Ser Ile Ala Cys Thr Val Ala Ala Phe Gly Ser Asp Pro
 595 600 605
 Gln Gly Asn Pro Asn Lys Cys Ser Tyr Lys Arg

610

615

<210> 39
<211> 1077
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 39

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gccgtggta gctgcgcggc gggggccggta tcagcgcagc agccggcgc atggagcacg
gccatcgta agcaggagga gagcgcgttc gcctcccgta cgatgcgcag cgtcgccgac
aacgtcgta gccatcagtc ggccgaaggc ggctggctta agaacaccaa tctggggcg
ccgccccatcgta ggcggcgcc ggagggcgta gccaatacga tcgacaatga tgcgacgacg
ctgccccatcgta agtttctggc gcgtgtgatc cacgcccggc gcgtccgata caagccggcc
ttcgagcgta ggctggattta tctgcttgcg gtcagttacg cgaacggcg ctggccgca
ttctatccgc tgccgggggg ctattacgat cacgtgacgt tcaacgacga cgccatgatc
cggggtatgta ttctgtctggc cgcaatggcg cgccgggggg cgccctatga atttgcac
gccccggcgcc ggcgcgcgc tgcagccgta gtcgagcgcc gcctggcgct catcctgcgc
acgcagatcc ggcaaggcgcc ggctgtacg gtctggcgta cgcaatgtga cagcgcacc
ttgcagccccg cctggcgccg cgcctatgag ccggcgcccc tgccggcgcc gggaaagtgt
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gacggcgctg tggcatggct ggcgcggcc gccattggcg gcgtgcgcgt ggagaatttc
acggacgccc acggccgccc tgaccggccg gccgtggccg acggccgccc gccggccgatc
tggcgccgt tctacgaggta cggcgccaa cggccgatct tccctggcg tgattccgtt
tttcaactaca cgttcgagaa aatcgagcgc gaggctacaa ttattacgg
tactggcgcc gctccgtgtt ggaagactat ccggccctggc ggcgcgcgt ggcgtat

60
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180
240
300
360
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660
720
780
840
900
960
1020
1077

<210> 40
<211> 358
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<221> DOMAIN
<222> (33)...(358)
<223> Catalytic domain

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<400> 40
Met Ala Pro Ile Leu Arg Pro Asn Leu Leu Cys Thr Tyr Ala Leu Cys
   1           5           10           15
Met Gly Leu Leu Ala Val Val Ser Cys Ala Ala Gly Pro Val Ser Ala
   20          25          30
Gln Gln Pro Ala Pro Trp Ser Thr Ala Ile Val Glu Gln Glu Glu Ser
   35          40          45
Ala Phe Ala Ser Pro Ser Met Arg Ser Val Ala Asp Asn Val Val Arg
   50          55          60
His Gln Ser Ala Glu Gly Gly Trp Pro Lys Asn Thr Asn Leu Ala Ala
   65          70          75          80
Pro Pro Ser Gly Pro Ala Pro Glu Gly Val Ala Asn Thr Ile Asp Asn
   85          90          95
Asp Ala Thr Thr Leu Pro Met Glu Phe Leu Ala Arg Val Ile His Ala

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100	105	110
Gly	Gly	
Val	Arg	
Tyr	Lys	
Pro	Ala	Phe
		Glu
		Arg
		Gly
		Leu
		Asp
		Tyr
115	120	125
Leu	Ala	Ala
Gln	Tyr	Ala
		Asn
		Gly
		Trp
		Pro
		Gln
		Phe
		Tyr
130	135	140
Arg	Gly	Gly
Tyr	Tyr	Asp
		His
		Val
		Thr
		Phe
		Asn
		Asp
		Asp
		Ala
		Met
145	150	155
Arg	Val	Met
Ile	Leu	Leu
Gly	Ala	Val
		Ala
		Arg
		Gly
		Gly
		Ala
		Pro
		Tyr
165	170	175
Glu	Phe	Val
Asp	Ala	Gly
		Arg
		Ala
		Arg
		Ala
		Ala
		Ala
180	185	190
Arg	Gly	Leu
Ala	Leu	Ile
Leu	Arg	Thr
		Gln
		Ile
		Arg
		Gln
		Gly
195	200	205
Leu	Thr	Val
Trp	Cys	Ala
		Gln
		Tyr
		Asp
		Ser
		Ala
		Thr
		Leu
		Gln
		Pro
210	215	220
Trp	Ala	Arg
Ala	Tyr	Glu
		Pro
		Pro
		Ser
		Leu
		Ser
225	230	235
Gly	Ile	Val
Arg	Tyr	Leu
		Met
		Ser
		Ile
		Asp
		His
		Pro
		Ser
		Pro
245	250	255
Val	Ala	Ala
Ala	Val	Asp
		Gly
		Ala
		Val
		Trp
		Leu
		Arg
		Ala
		Ala
260	265	270
Ala	Gly	Val
		Arg
		Val
		Glu
		Asn
		Phe
		Thr
		Asp
275	280	285
Arg	Arg	Ala
Ala	Val	Ala
		Asp
		Ala
		Gly
		Ala
		Pro
290	295	300
Tyr	Glu	Phe
Gly	Ala	Asn
		Arg
		Pro
		Ile
		Phe
305	310	315
Phe	His	Tyr
		Phe
		Gly
		Gl
		Leu
		Arg
		Glu
		Arg
		Arg
		Ala
		Gly
325	330	335
Asn	Tyr	Tyr
Gly	Tyr	Trp
		Ala
		Arg
		Ser
		Val
		Leu
		Glu
		Asp
		Tyr
340	345	350
Trp	Arg	Ala
		Arg
		Val
355		

<210> 41

<211> 1080

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 41

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gtaagcgaag	aagccaaaaa	aatagccgaa	aatgtttgt	tatatcaacg	cgatattgg	180
ggttggccaa	aaaacactga	aattcaaaat	gaactttcag	aaaaagaaaa	actaacatta	240
aaagaattaa	aatcgatcc	aaaaggatgt	accatcgaca	atggtgcaac	gtgtcagggaa	300
ttactttct	tatccaaaat	atataaatcc	aatccagatg	agcgatataa	aatggcttc	360
ttaaaagg	tgatttac	gattacagct	caataaaaa	atggtggtt	gccacaatat	420
tacccttga	gagaaggata	ttacactcat	attacttaca	acgataatgc	aatggtgaat	480
gttttaaagt	tgttggaaaga	agttaaagat	aaatctgatt	actactcaat	tcaagcaccc	540
gatgaaattt	ccaaaatggc	tgaagtatca	ttaataaaag	gagtcgattt	catattaaaa	600
acacagtaca	aacaaaatgg	aatattaacc	gcttgggt	cacaacatga	caggaaaca	660
ttgaaacctg	ctaaagcaag	agcttatgaa	ttgccttcgt	taagcggaaa	agaatcagcc	720
aaaattgtgt	tgttattaaat	gtcaatcgaa	aatccatcta	aagaagtaat	tactgccgt	780
aattcagcag	ttaattgggt	tgaaaaaaaca	aaaatcaacg	gaattaaaaat	tgaaaccatt	840
tccaccggga	aaaaggatga	aaaagataga	attgtgtt	aaagtcctga	tgctccgccc	900
cttgggcaa	gatttatgga	attaagtgac	aacaaaccat	tttttgtga	tcgtacggaa	960

aagaaaaaat acagcatgtc agaaattagt caagagcgta gaaccggcta tgcatgtac 1020
 accaacgaac caaaagaagt tttaaaaaaa tacgatgatt ggaagtcatc attaaactaa 1080
 <210> 42
 <211> 359
 <212> PRT
 <213> Unknown
 <220>
 <223> Obtained from an environmental sample
 <221> SIGNAL
 <222> (1)...(21)
 <221> DOMAIN
 <222> (22)...(359)
 <223> Catalytic domain
 <400> 42
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 Met Asn Val Phe Thr Gln Glu Lys Lys Val Thr Trp Lys Ser Ile Thr
 20 25 30
 Glu Asn Asn Asp Glu Asn Trp Phe Val Ser Glu Glu Ala Lys Lys Ile
 35 40 45
 Ala Glu Asn Val Leu Leu Tyr Gln Arg Asp Ile Gly Gly Trp Pro Lys
 50 55 60
 Asn Thr Glu Ile Gln Asn Glu Leu Ser Glu Lys Glu Lys Leu Thr Leu
 65 70 75 80
 Lys Glu Leu Lys Ser Asp Pro Lys Gly Cys Thr Ile Asp Asn Gly Ala
 85 90 95
 Thr Cys Gln Glu Leu Leu Phe Leu Ser Lys Ile Tyr Lys Ser Asn Pro
 100 105 110
 Asp Glu Arg Tyr Lys Met Ala Phe Leu Lys Gly Val Ile Tyr Leu Ile
 115 120 125
 Thr Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Leu Arg
 130 135 140
 Glu Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn
 145 150 155 160
 Val Leu Lys Leu Leu Lys Glu Val Lys Asp Lys Ser Asp Tyr Tyr Ser
 165 170 175
 Ile Gln Ala Pro Asp Glu Ile Ser Lys Met Ala Glu Val Ser Phe Asn
 180 185 190
 Lys Gly Val Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Asn Gly Ile
 195 200 205
 Leu Thr Ala Trp Cys Ala Gln His Asp Arg Glu Thr Leu Lys Pro Ala
 210 215 220
 Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu Ser Gly Lys Glu Ser Ala
 225 230 235 240
 Lys Ile Val Leu Leu Met Ser Ile Glu Asn Pro Ser Lys Glu Val
 245 250 255
 Ile Thr Ala Val Asn Ser Ala Val Asn Trp Phe Glu Lys Thr Lys Ile
 260 265 270
 Asn Gly Ile Lys Ile Glu Thr Ile Ser Thr Gly Lys Lys Asp Glu Lys
 275 280 285
 Asp Arg Ile Val Val Glu Ser Pro Asp Ala Pro Pro Leu Trp Ala Arg
 290 295 300
 Phe Met Glu Leu Ser Asp Asn Lys Pro Phe Phe Cys Asp Arg Asp Gly
 305 310 315 320

Lys Lys Lys Tyr Ser Met Ser Glu Ile Ser Gln Glu Arg Arg Thr Gly
 325 330 335
 Tyr Ala Trp Tyr Thr Asn Glu Pro Lys Glu Val Leu Lys Lys Tyr Asp
 340 345 350
 Asp Trp Lys Ser Ser Leu Asn
 355

<210> 43

<211> 1902

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 43

gtggatccaa	agaattgggg	cagcggattt	accggcgaaa	tcaaagtaac	taacaacaca	60
agccaaacag	tcaatagctg	gtctgtgtca	tggcaagagg	caggagccag	tgtaactaat	120
tccttggatg	caaccttggg	aggacgaat	ccttataccg	caaccgggtt	aggatggAAC	180
tcaaccctgg	cggccggagc	ctctggcagt	tttgggtttc	aagcaaacgg	cactgcgggg	240
gcacccaaagg	taaatggcag	tttgtgtgg	gcgactgcat	catctgcagc	gaccagcaaa	300
tccagtgcga	gtgttgcgag	ttcaaagatt	gcaagttcaa	ttcaatcaag	tgcaactagc	360
agttcaaaat	cgtccagttc	tgtgcaccc	tcaagcacgc	caaaatccag	tagctctgct	420
ccaaacggctg	catcatccac	tattcaagaa	gagcaagccg	gttttgccg	tgttagacgg	480
attgcaacgg	aaagtaccaa	caccggattc	accggcaacg	gtcacaccaa	ttccaaataat	540
gtacaagggtg	ctgccattgt	gtggggcggt	aatgcaacta	ccagtgcacg	ccataacaatt	600
actttccgct	tcgctaattgg	tggcaactgc	aatcgcaatg	gctcgctagt	cattaacggc	660
ggcagcaatg	gtatttacac	ggtgcattta	ccacgcaccc	cgagctgggc	tgactggcaa	720
acagtaagtc	tggaaattga	tttgttacaa	ggcaataaca	atttgcac	caccgcattt	780
actgcagatg	gcctcgcaaa	tatcgacttc	atcaaatttgc	aaggagcatc	aaccaaagcg	840
ggaacctgtg	caggtgcgg	cagcagtagc	agtgttgcct	cttcggtaaa	atccagtgt	900
agcgcggcaa	gcagttctgt	accaacgaaac	accggcgcc	tgctaactt	ggatggcaac	960
cctggcgcaa	gttggcttaa	caaatcgct	acaaagtgg	gcccgcgc	cgctgcac	1020
gttgcctt	atcaacagt	caacggcg	tggccaaaaa	atctggatta	caattcagt	1080
agcgtggta	atggcggcag	tgcacggc	accatcgata	atggtgcac	tattactgaa	1140
atgtttatc	tcgctgaggt	ttacaaaacc	ggaaacaaata	ccaagtacc	cgatgcagtt	1200
cgcgtgcag	caaactttat	cgtgagttc	caatatacg	ctggcgcgtt	gccgcaattt	1260
tatccgctca	aagggtgcta	tgcagaccac	gccaccc	atgataacgg	catggcttac	1320
gcattaaact	tattggattt	cgtgcacaaac	aagcgcgc	ctttgatac	ggatgtctt	1380
aatgacacag	accgcgc	attaaaaca	gcccgtt	aagggttttgc	ttacatttt	1440
aaagcgcac	ggaaacaaaa	tggaaaattt	acagcgtt	gcccacaaca	ttggcgcact	1500
gactatcaac	ctaaaaaaagc	acgcgtt	gaatttggat	cactgagtgg	tagcgtgt	1560
gttgggtttaa	ttgcatttt	aatgacgcag	ccgcagacag	cacaaatcca	aacggccgtt	1620
aaagcaggcc	tcaactgtt	caatagcccg	agcacctatt	tggaaaggta	cacctacgt	1680
tcatccaaag	cgtccactaa	tccatagtg	cagaaagccg	gaagtagaaat	gtggatcg	1740
ttttacgatt	taataccaa	ccgtggttt	ttcagcgacc	gggacggca	caaattctat	1800
gacattacca	aatgtctga	agaaacgtcgc	acgggtata	gttgggttgg	cgcttatgtt	1860
gagagcatca	tcgccttgg	caaaaaagt	ggctatctat	aa		1902

<210> 44

<211> 633

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> BINDING

<222> (4)...(89)

<223> Carbohydrate binding module

<221> BINDING

<222> (152)...(275)

<223> Carbohydrate binding module

<221> DOMAIN

<222> (277)...(633)

<223> Catalytic domain

<400> 44

Met	Asp	Pro	Lys	Asn	Trp	Gly	Ser	Gly	Phe	Thr	Gly	Glu	Ile	Lys	Val
1					5				10				15		
Thr	Asn	Asn	Thr	Ser	Gln	Thr	Val	Asn	Ser	Trp	Ser	Val	Ser	Trp	Gln
					20				25				30		
Glu	Ala	Gly	Ala	Ser	Val	Thr	Asn	Ser	Trp	Asn	Ala	Thr	Leu	Gly	Gly
					35				40				45		
Thr	Asn	Pro	Tyr	Thr	Ala	Thr	Gly	Leu	Gly	Trp	Asn	Ser	Thr	Leu	Ala
					50				55				60		
Pro	Gly	Ala	Ser	Ala	Ser	Phe	Gly	Phe	Gln	Ala	Asn	Gly	Thr	Ala	Gly
	65					70				75			80		
Ala	Pro	Lys	Val	Asn	Gly	Ser	Leu	Cys	Gly	Ala	Thr	Ala	Ser	Ser	Ala
					85				90				95		
Ala	Thr	Ser	Lys	Ser	Ser	Ala	Ser	Val	Ala	Ser	Ser	Lys	Ile	Ala	Ser
					100				105				110		
Ser	Ile	Gln	Ser	Ser	Ala	Thr	Ser	Ser	Ser	Lys	Ser	Ser	Ser	Ser	Ala
					115				120				125		
Ala	Pro	Ser	Ser	Thr	Pro	Lys	Ser	Ser	Ser	Ser	Ala	Pro	Thr	Ala	Ala
					130				135				140		
Ser	Phe	Thr	Ile	Gln	Glu	Glu	Gln	Ala	Gly	Phe	Cys	Arg	Val	Asp	Gly
	145					150				155			160		
Ile	Ala	Thr	Glu	Ser	Thr	Asn	Thr	Gly	Phe	Thr	Gly	Asn	Gly	Tyr	Thr
						165				170			175		
Asn	Ser	Asn	Asn	Val	Gln	Gly	Ala	Ala	Ile	Val	Trp	Ala	Val	Asn	Ala
					180				185				190		
Thr	Thr	Ser	Ala	Arg	His	Thr	Ile	Thr	Phe	Arg	Phe	Ala	Asn	Gly	Gly
					195				200				205		
Thr	Ala	Asn	Arg	Asn	Gly	Ser	Leu	Val	Ile	Asn	Gly	Gly	Ser	Asn	Gly
					210				215				220		
Asn	Tyr	Thr	Val	Gln	Leu	Pro	Arg	Thr	Ala	Ser	Trp	Ala	Asp	Trp	Gln
	225					230				235			240		
Thr	Val	Ser	Leu	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Asn	Leu	Gln
					245				250				255		
Leu	Thr	Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Phe	Ile	Lys
					260				265				270		
Ile	Glu	Gly	Ala	Ser	Thr	Lys	Ala	Gly	Thr	Cys	Ala	Gly	Ala	Val	Ser
					275				280				285		
Ser	Ser	Ser	Val	Ala	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ala	Ala	Ser
					290				295				300		
Ser	Ser	Val	Pro	Thr	Asn	Thr	Gly	Ala	Met	Leu	Thr	Leu	Asp	Gly	Asn
	305					310				315			320		
Pro	Ala	Ala	Ser	Trp	Leu	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Ser	Ala	Ser
					325				330				335		
Arg	Ala	Asp	Ile	Val	Ala	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro
					340				345				350		
Lys	Asn	Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Ala
					355				360				365		
Ser	Gly	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu
	370					375				380					

Ala Glu Val Tyr Lys Thr Gly Asn Asn Thr Lys Tyr Arg Asp Ala Val
 385 390 395 400
 Arg Arg Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala
 405 410 415
 Leu Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr
 420 425 430
 Phe Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala
 435 440 445
 Ala Asn Lys Arg Ala Pro Phe Asp Thr Asp Val Phe Asn Asp Thr Asp
 450 455 460
 Arg Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Val Asp Tyr Ile Leu
 465 470 475 480
 Lys Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln
 485 490 495
 His Gly Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu
 500 505 510
 Glu Ser Leu Ser Gly Ser Glu Ser Val Gly Val Ile Ala Phe Leu Met
 515 520 525
 Thr Gln Pro Gln Thr Ala Gln Ile Gln Thr Ala Val Lys Ala Gly Leu
 530 535 540
 Asn Trp Phe Asn Ser Pro Ser Thr Tyr Leu Glu Gly Tyr Thr Tyr Asp
 545 550 555 560
 Ser Ser Lys Ala Ser Thr Asn Pro Ile Val Gln Lys Ala Gly Ser Arg
 565 570 575
 Met Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser
 580 585 590
 Asp Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Lys Met Ser Glu Glu
 595 600 605
 Arg Arg Thr Gly Tyr Ser Trp Gly Gly Ala Tyr Gly Glu Ser Ile Ile
 610 615 620
 Ala Phe Gly Lys Lys Val Gly Tyr Leu
 625 630

<210> 45
 <211> 987
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 45
 atgactagac ggcgcattcat cgcgttatac tgtttcttcg cggccgtctg cgccgcacgcg 60
 cagtccacccg tgcgctggaa ggacgtgctc gagcagtccg agggctggta ttccacgacc 120
 gccgcgcacg tcgtcgccga cacgggtctg ctgtatcaac gtccatccgg tggatggccg 180
 aaggacatcg acatgacggc gccgcggcg gaccgcactc ctcccgccgc tccagacgcg 240
 accatcgaca acggcgcac gaccacgcag atccgcctgc tcgctcggtc ggcctcgccg 300
 gcaccggcg ctggcccca cacctacacg gcggccggcgc ttcgcggat cgattacctg 360
 ctcgaggcgc agtataccaa cggcggttgg ccgcagttct tccccctgcg caaggactat 420
 tcgcgtctacg tcacgttcaa cgacgacgcg atgatgaacg tgatgttctt gctgacgcg 480
 gtctcggcg gagatgcgc gttcacgttc gtggacgaac aacgcgcga ccgcgcgcgc 540
 gctgccgtcg ccaagggggt ctccgtcattc ctgaagtcgc aggtccggat cgacggacg 600
 ctgaccgcctt ggtgcgcgc acacgacgag atcacccctgg caccgcgtcc ggcgcgcacc 660
 ttgcgacacg cgtcgctcag cggcaacgag tctgtcgca tcgtgcgtt cctgtatgacc 720
 cgtccgcgcga cgccagcgtat cgtcgccgcgt gtcgtgcgg cggtcgcctg gtcagacgc 780
 gtccgcctcc ctgacggacg gtggcccgta ttctacgagt tcggtaccaa tcgtccgatc 840
 ttctcggggc gagacagtgt cgtgcgtacaa aactcgagg agatcgaaca ggaacgtcag 900
 gagggtacacg cgtggtaacgg cacgtggccg aggacgcttg ttgagaagat gtaccctgca 960
 tggaaagtcgc ggcttcggg caagtag 987

<210> 46
<211> 328
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(20)

<221> DOMAIN
<222> (21)...(328)
<223> Catalytic domain

<400> 46
Met Thr Arg Arg Ala Phe Ile Ala Val Ile Cys Phe Phe Ala Ala Val
1 5 10 15
Cys Ala His Ala Gln Ser Thr Val Arg Trp Lys Asp Val Leu Glu Gln
20 25 30
Ser Glu Gly Trp Tyr Ser Thr Thr Ala Ala His Val Val Ala Asp Thr
35 40 45
Val Leu Leu Tyr Gln Arg Pro Ser Gly Gly Trp Pro Lys Asp Ile Asp
50 55 60
Met Thr Ala Pro Pro Ala Asp Arg Thr Pro Pro Ala Arg Pro Asp Ala
65 70 75 80
Thr Ile Asp Asn Gly Ala Thr Thr Gln Ile Arg Leu Leu Ala Arg
85 90 95
Ala Ala Ser Gly Ala Pro Ala Ala Ala Ala His Thr Tyr Thr Ala Ala
100 105 110
Ala Leu Arg Gly Ile Asp Tyr Leu Leu Glu Ala Gln Tyr Pro Asn Gly
115 120 125
Gly Trp Pro Gln Phe Phe Pro Leu Arg Lys Asp Tyr Ser Arg Tyr Val
130 135 140
Thr Phe Asn Asp Asp Ala Met Met Asn Val Met Phe Leu Leu Asp Glu
145 150 155 160
Val Ser Ala Gly Asp Ala Pro Phe Thr Phe Val Asp Glu Gln Arg Arg
165 170 175
Asp Arg Ala Arg Ala Ala Val Ala Lys Gly Val Ser Val Ile Leu Lys
180 185 190
Ser Gln Val Arg Ile Asp Gly Thr Leu Thr Ala Trp Cys Ala Gln His
195 200 205
Asp Glu Ile Thr Leu Ala Pro Arg Pro Ala Arg Thr Phe Glu His Ala
210 215 220
Ser Leu Ser Gly Asn Glu Ser Val Ala Ile Val Arg Phe Leu Met Thr
225 230 235 240
Arg Pro Pro Thr Pro Ala Ile Val Ala Ala Val Asp Ala Ala Val Ala
245 250 255
Trp Leu Arg Arg Val Arg Leu Pro Asp Gly Arg Trp Ala Arg Phe Tyr
260 265 270
Glu Phe Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Ser Val Val
275 280 285
Arg Tyr Lys Leu Glu Glu Ile Glu Gln Glu Arg Gln Glu Gly Tyr Ala
290 295 300
Trp Tyr Gly Thr Trp Pro Arg Thr Leu Val Glu Lys Met Tyr Pro Ala
305 310 315 320
Trp Lys Ser Arg Leu Pro Gly Lys
325

<210> 47
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 47

ataaaaaatt taaaaaatat	tgttaggagcg ttacttatat	ctgttaacgtt ttgtgtgcac	60
ggcaggtaa acaaaaaatc	ctggcgggctt attacacagt	ctaacgacga tgcatggttt	120
gcacatctgatg gagctgcaca	gattgcagat aatgtattac	tctatcagcg caatgttggc	180
ggatggctta aaaatattga	aatgcaggaa ccgcttagt	aggccgacaa aaaaaagctg	240
atagatctta agtctacggc	caaagaaagt actacagata	atggggctac gtgtcaggaa	300
atggatttcc tctctaaat	atataaaacaa aagccgaag	agaagtataa agaggctttt	360
ttaaaaggac ttaatttattt	gcttgaagca cagtataaaa	atgggtggatg gccacagttc	420
taccctttaa aaaaaggta	ttatacccac attacctata	atgacgatc tatgttaaac	480
attcttatga tcttaaagaa	tattaaggaa gatgccaact	attacagtat tacgccaagc	540
gataaaagttt taaagcaggt	atcgacagct tttgacagag	gcattgactg cattctaaaa	600
acacagtaca agcaaaaagg	tgtgcttaca agctgggtg	cccagcacga tgaggttaca	660
ttagaacctg caaatgcaag	ggcttttgag ttggcatcac	taagtggtaa agaatctgct	720
aaaataaacgt tggctgtaat	gtctgtaaaa aatccgtcta	aagagggtgt tgctgctgta	780
gatgctgctg tggcgtgggtt	tggaaaaaca aaaattgaag	gcattaaagt agaagaagta	840
accggagctg atggcaaaaa	ggatagggtt gtagtacaaa	gggctgatgc cgaaccattg	900
tggcgcgtt ttatgaaact	ggataccaac aggccatttt	tttgcacag ggacggtata	960
aaaaaatatt cgcttgctga	gataggtcat gaacccgta	acggatatgg ctggtacacc	1020
aacgaaccaa aagaagttt	accaaatac accaaatgga	aaaacagttct taaatag	1077

<210> 48
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(358)
 <223> Catalytic domain

<400> 48

Met Lys Asn Phe Lys Asn Ile Val Gly Ala Leu Leu Ile Ser Val Thr			
1	5	10	15
Phe Cys Val His Gly Gln Val Asn Lys Lys Ser Trp Arg Ala Ile Thr			
20	25	30	
Gln Ser Asn Asp Asp Ala Trp Phe Ala Ser Asp Gly Ala Ala Gln Ile			
35	40	45	
Ala Asp Asn Val Leu Leu Tyr Gln Arg Asn Val Gly Gly Trp Pro Lys			
50	55	60	
Asn Ile Glu Met Gln Glu Pro Leu Ser Glu Ala Asp Lys Lys Lys Leu			
65	70	75	80
Ile Asp Leu Lys Ser Thr Ala Lys Glu Ser Thr Thr Asp Asn Gly Ala			
85	90	95	
Thr Cys Gln Glu Met Val Phe Leu Ser Lys Ile Tyr Lys Gln Lys Pro			
100	105	110	

Glu Glu Lys Tyr Lys Glu Ala Phe Leu Lys Gly Leu Asn Tyr Leu Leu
 115 120 125
 Glu Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Lys
 130 135 140
 Lys Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asp Ser Met Val Asn
 145 150 155 160
 Ile Leu Met Ile Leu Lys Asn Ile Lys Glu Asp Ala Asn Tyr Tyr Ser
 165 170 175
 Ile Thr Pro Ser Asp Lys Val Leu Lys Gln Val Ser Thr Ala Phe Asp
 180 185 190
 Arg Gly Ile Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Lys Gly Val
 195 200 205
 Leu Thr Ser Trp Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Ala
 210 215 220
 Asn Ala Arg Ala Phe Glu Leu Ala Ser Leu Ser Gly Lys Glu Ser Ala
 225 230 235 240
 Lys Ile Thr Leu Leu Met Ser Val Lys Asn Pro Ser Lys Glu Val
 245 250 255
 Val Ala Ala Val Asp Ala Ala Val Ala Trp Phe Glu Lys Thr Lys Ile
 260 265 270
 Glu Gly Ile Lys Val Glu Glu Val Thr Gly Ala Asp Gly Lys Lys Asp
 275 280 285
 Arg Val Val Val Gln Arg Ala Asp Ala Glu Pro Leu Trp Ala Arg Phe
 290 295 300
 Met Glu Leu Asp Thr Asn Arg Pro Phe Phe Cys Asp Arg Asp Gly Ile
 305 310 315 320
 Lys Lys Tyr Ser Leu Ala Glu Ile Gly His Glu Arg Arg Asn Gly Tyr
 325 330 335
 Gly Trp Tyr Thr Asn Glu Pro Lys Glu Val Leu Lys Lys Tyr Thr Lys
 340 345 350
 Trp Lys Asn Ser Leu Lys
 355

<210> 49

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 49

atgtaagtt	tcatcgccgt	atcagtgtt	cataattact	gcacagggca	gacagcgtcc	60
acccaaaatt	cagtggccga	aaagatgctt	cagtaccagt	tgtcaatgg	cgcctggccc	120
aaacagttgg	tagacaaaag	tgtcggtat	tacagtcttc	cattaacgaa	agagcgccta	180
cagcagatca	agaaaacaga	tattgtatcat	gctacgctcg	acaacagtgc	gacaacccgg	240
gaaataactg	aattgtatcaa	ggcttttaag	gacactaaa	ataaggcata	tttgactgct	300
gtagaaaaagg	ggattgcata	tattttatcg	gctcaatatg	agaatggcg	atttccacaa	360
tactacccaa	ataaattata	ctatagagct	gagataacat	acaacgatga	tgcgatgatc	420
aatgcattac	tagtgcctt	caaagtagcc	aataagcgg	aggggttta	ggctatcaat	480
cccatatttg	tgtcaaaaagc	gcaaaaaagca	gttggaaaagg	gtataacctg	tatcctaaaa	540
acacagggtca	tacaagacgg	aaaaaggagt	atttgggctg	cgcaatacga	tcagaacact	600
ttacaacctg	ctcaggcaag	aaagttgaa	ccagcttcat	tgagcacaag	tgaatctgtt	660
tccatcggtt	gctttctcat	gctacagcct	gcaaccactg	aaattaagca	agcgatcgaa	720
catgcaatac	aatggttcga	acagcatgat	attgaagggt	accgtttcga	ccgcatacaa	780
gatagggtga	ctggaaaata	tcaacggcaa	cttgcgcag	atcggacttc	cacgatttg	840
gcccgtttt	ataatctcgaa	agacaaccgc	ccattgtttg	gagatggga	caataacaatc	900
aaatacaact	ttgaggaggt	ttcagaggag	cgtaaaaatg	gctatgctt	gttcggcaac	960
tggccggaaa	agctgatcca	aaaggactat	ccaaaatgga	aaaaacaata	caaaattaaa	1020

taa

1023

<210> 50
<211> 340
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(16)

<221> DOMAIN
<222> (17)...(340)
<223> Catalytic domain

<400> 50
Met Leu Ser Phe Ile Ala Val Ser Val Phe His Asn Tyr Cys Thr Gly
1 5 10 15
Gln Thr Ala Ser Thr Lys Asn Ser Val Ala Glu Lys Met Leu Gln Tyr
20 25 30
Gln Leu Ser Asn Gly Ala Trp Pro Lys Gln Leu Val Asp Lys Ser Val
35 40 45
Val Asp Tyr Ser Leu Pro Leu Thr Lys Glu Arg Leu Gln Gln Ile Lys
50 55 60
Lys Thr Asp Ile Asp His Ala Thr Leu Asp Asn Ser Ala Thr Thr Arg
65 70 75 80
Glu Ile Thr Glu Leu Ile Lys Ala Phe Lys Asp Thr Lys Asn Lys Ala
85 90 95
Tyr Leu Thr Ala Val Glu Lys Gly Ile Ala Tyr Ile Leu Ser Ala Gln
100 105 110
Tyr Glu Asn Gly Phe Pro Gln Tyr Tyr Pro Asn Lys Leu Tyr Tyr
115 120 125
Arg Ala Glu Ile Thr Tyr Asn Asp Asp Ala Met Ile Asn Ala Leu Leu
130 135 140
Val Leu Tyr Lys Val Ala Asn Lys Arg Glu Gly Phe Glu Ala Ile Asn
145 150 155 160
Pro Ile Phe Val Ser Lys Ala Gln Lys Ala Val Glu Lys Gly Ile Thr
165 170 175
Cys Ile Leu Lys Thr Gln Val Ile Gln Asp Gly Lys Arg Ser Ile Trp
180 185 190
Ala Ala Gln Tyr Asp Gln Asn Thr Leu Gln Pro Ala Gln Ala Arg Lys
195 200 205
Phe Glu Pro Ala Ser Leu Ser Thr Ser Glu Ser Val Ser Ile Val Arg
210 215 220
Phe Leu Met Leu Gln Pro Ala Thr Thr Glu Ile Lys Gln Ala Ile Glu
225 230 235 240
His Ala Ile Gln Trp Phe Glu Gln His Asp Ile Glu Gly Tyr Arg Phe
245 250 255
Asp Arg Ile Gln Asp Arg Val Thr Gly Lys Tyr Gln Arg Gln Leu Val
260 265 270
Ala Asp Arg Thr Ser Thr Ile Trp Ala Arg Phe Tyr Asn Leu Glu Asp
275 280 285
Asn Arg Pro Leu Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Asn Phe
290 295 300
Glu Glu Val Ser Glu Glu Arg Arg Asn Gly Tyr Ala Trp Phe Gly Asn
305 310 315 320
Trp Pro Glu Lys Leu Ile Gln Lys Asp Tyr Pro Lys Trp Lys Lys Gln

325
Tyr Lys Ile Lys
340

330

335

<210> 51
<211> 1131
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 51

gtgacgtggg atcagatcct tcgtcagcct	gcccgcctgggt	acggcggtcc	ggaagcgcga	60
cgcatcgcgaa atctggctct	gtgttaccag	cgcgcgacgg	ggggctggcc	120
gacatggcgcc	ggtcgttgcc	tccggacgat	cgcacgacgc	180
accgactcgaa	cgatcgacaa	tggatcgacg	acgacgcagt	240
cagcacgccc	agcaggacc	cgtgcgcgac	gccatcacgc	300
aacgcgcaat	actcgaacgg	cgtatggccg	cgtactttc	360
cgtcacatca	cgttcaacga	cgacgcgatg	atcaatgtaa	420
gcagaagctc	gcatgcctt	cgaaggggatc	gacgcgggtcc	480
gccatcacgc	gtggcatcga	cgtgttctc	gtcggggaccg	540
acgggctgggt	gccagcaga	tgacgagcgc	ttccctcgccc	600
gagcacccat	cgatcggccag	caaggaaacg	ccaccaaggc	660
gatcgccccg	gtcagcagat	catcgccggc	gtacgggtcc	720
gcgaccctgt	cgggtgtcg	atcgaggccg	ctgtcgagtg	780
gacgtcgtcg	ccgcgcggaa	atcgaggccg	gttgcgcgtg	840
ggcacgaaacc	gccaatgtt	ttccggccgc	ccaccaaggc	900
atcgagatgtt	agcgcgcac	cgctacagc	gtacgggtcc	960
aacgaggagt	atccggcg	tggatggccg	actatgcgc	1020
cacaaggagt	ccggtaagt	cgacacacg	gcatcgtgc	1080
gtcgaagaca	aagaccagcc	gcagccgaaa	acatcttgc	
		gtgtttcg	ctggggcggt	1131

<210> 52
<211> 376
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(376)
<223> Catalytic domain

<400> 52

Met	Thr	Trp	Asp	Gln	Ile	Leu	Arg	Gln	Pro	Ala	Ala	Trp	Tyr	Gly	Gly
1				5				10				15			
Pro	Glu	Ala	Arg	Arg	Ile	Ala	Asn	Leu	Val	Leu	Leu	Tyr	Gln	Arg	Ala
					20				25			30			
Thr	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Ala	Arg	Ser	Leu	Ser	Pro
					35			40			45				
Asp	Asp	Arg	Thr	Thr	Leu	Ala	Ala	Glu	Arg	Ala	Leu	Thr	Asp	Ser	Thr
					50			55			60				
Ile	Asp	Asn	Gly	Ser	Thr	Thr	Thr	Gln	Leu	Arg	Phe	Leu	Ala	Met	Val
					65			70			75			80	
Gln	His	Ala	Gln	Gln	Ala	Pro	Val	Arg	Asp	Ala	Ile	Thr	His	Gly	Leu
						85			90			95			
Asp	Tyr	Leu	Leu	Asn	Ala	Gln	Tyr	Ser	Asn	Gly	Gly	Trp	Pro	Gln	Tyr

100	105	110													
Phe	Pro	Leu	Arg	Asp	Asp	Tyr	Ser	Arg	His	Ile	Thr	Phe	Asn	Asp	Asp
115						120						125			
Ala	Met	Ile	Asn	Val	Met	Thr	Val	Leu	Arg	Asp	Val	Ala	Glu	Ala	Arg
130						135						140			
Met	Pro	Phe	Glu	Gly	Ile	Asp	Ala	Val	Arg	Arg	Asp	Arg	Ala	Arg	Val
145						150					155				160
Ala	Ile	Thr	Arg	Gly	Ile	Asp	Val	Ile	Leu	Gly	Thr	Gln	Ile	Arg	Val
						165					170				175
Gly	Asp	Arg	Leu	Thr	Gly	Trp	Cys	Gln	Gln	His	Asp	Glu	Arg	Ser	Leu
						180					185				190
Ala	Pro	Thr	Lys	Ala	Arg	Ala	Tyr	Glu	His	Pro	Ser	Ile	Ala	Ser	Lys
						195					200				205
Glu	Thr	Val	Thr	Ile	Thr	Arg	Phe	Leu	Met	Thr	Leu	Asp	Arg	Pro	Ser
						210					215				220
Gln	Gln	Ile	Ile	Ala	Ala	Ile	Glu	Ala	Ala	Val	Glu	Trp	Leu	Arg	Val
						225					230				240
Ala	Thr	Leu	Ser	Gly	Val	Arg	Val	Glu	Arg	Arg	Pro	Asp	Pro	Ala	Ser
						245					250				255
Pro	Thr	Gly	Tyr	Asp	Val	Val	Ala	Ala	Pro	Asp	Ala	Ala	Ala	Pro	Pro
						260					265				270
Thr	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Met	Phe	Ser
						275					280				285
Gly	Arg	Asp	Gly	Val	Ile	Arg	Phe	Arg	Leu	Ala	Asp	Ile	Glu	Ile	Glu
						290					295				300
Arg	Arg	Thr	Gly	Tyr	Ser	Trp	Met	Gly	Asp	Tyr	Ala	Ala	Arg	Leu	Leu
						305					310				320
Asn	Glu	Glu	Tyr	Pro	Ala	Trp	Ala	Arg	Leu	Arg	Arg	Ala	Ser	Phe	Gln
						325					330				335
Asn	Ala	Glu	Leu	His	Lys	Glu	Ser	Gly	Glu	Val	Val	His	Thr	Ala	Ile
						340					345				350
Val	His	Asp	Leu	Ala	Phe	Leu	Asp	Val	Glu	Asp	Lys	Asp	Gln	Pro	Gln
						355					360				365
Pro	Lys	Val	Leu	Phe	Ala	Gly	Arg								
						370					375				

<210> 53

<211> 1977

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 53

atgaataact	caacaaaaaa	aatgattcgg	ccactcaagg	catctttgc	cttggcgct	60
ctcgcactgg	caatcgcatc	accctcatgg	gcggcttgct	cttacagcgt	aaccaataat	120
tggggctctg	gctttaccgg	agaaaattaaa	gtaacccaacg	atacaacatc	gactgtaaat	180
aattggctcg	tgtcttggca	ggaatcaggc	gtgaccgtca	ctaacgcatg	gaatgcaaca	240
ctgagcggat	caaattccta	taccgcaaca	tcactcgggt	ggaacggaaac	tctcgctcca	300
aaagcttcag	caagtttgg	tttcaagca	aatggAACAG	cgggcgcacc	gaaagtaaat	360
ggaaccttgt	gtggtaccag	cacatcatca	acaggtacat	cctcagttgc	actttcatcc	420
gtagcgagta	gcgttgcgt	atcaaggcgt	aaatcatcaa	gctctgttgc	aaccatcagt	480
agctctaaat	ccagcagcag	tgtgccgaca	gtttcatcat	tcactattca	ggaagagcaa	540
gccggtttct	gccgtgtaga	tgcattgca	actgaaagta	ctaacactgg	ctatacaggt	600
aatggctaca	ccaacaccac	taatgcgcaa	ggcgctgcaa	ttgaatgggc	aattaatgct	660
cccaacagca	gccgctacac	cctcaccttc	cgttatgcca	atgctgttac	cgctaattcgc	720
aatggttcgt	tattaattaa	cgacgaaagc	aatggtaact	acacagtgc	attgccaagt	780
accggcgcac	gggcaacctg	gcaaaaccgtc	agtgttgaag	tggatttgg	gcaaggcaat	840

aatattttga aactcgcttc gcttactgct gatggccttg cgaatataaga ttcattaaaa	900
attgaaggcg cacaagccaa agctggtga tgcagcacta cggtaagttag cagctcttcg	960
tcaattaaat caagtccag ttcatcatcg tccagctcaa ctgcagcaat aaaaacatta	1020
acactggatg gtaaccctgc tgcaaactgg ttataataat ccagaaccaa gtggaatgtc	1080
agcagagctg acatcgact ttctatcg caatcaaata gttggctggcc aaaaaatttg	1140
gactacaact cggtaggctc aggtatggt ggttagcaca gcggcactat tgataatgg	1200
gcaaccataa ccgaaatggt gtacctcgct gaagtgtata aaaatggcgg gaataccaaa	1260
taccgcgacg ccgtgcgcag agcagcgaat ttatgtga gttcacaata cagcactgg	1320
gcittaccgc agtttatcc gctgaaagggt gtttacgcag atcacgctac cttaatgat	1380
aatggtatgg cttacgcgtt gactgttctg gatttcgcgg taaataaaacg cgcgccattt	1440
gataacgata ttttctctga ctctgaccgc agcaaattta aactgttgt taccaaaggc	1500
gtcgattaca tattaaaagc gcaatggaaa cagaatggaa attaaccgt atgggtgcga	1560
caacacggtg ctaatgatta tcaaccgaaa aaagcgcgtg cttacgagtt agaatcattt	1620
agttgttagt aatctgtcg tttactcgct ttcttaatga ctcaaccaca aaccacgcaa	1680
attgaagcag ctgtgcgtgc aggtgtggcc tgggttataa gccaaggcac ctacttgaat	1740
aattacactt acgattttc caaagcttcg accaatccaa tcgtgcacaaa atccgaaagc	1800
aaaatgtggt atcgcttta tgacctgaat accaaccgcg gtttcttcag tgatcgtgac	1860
ggcagcaagt tctacgacat cacccaaata tcagaagagc gtcgcactgg ttacagttgg	1920
ggtgggtact acggcagctc gattatcagc ttgcacaaa aagtgggata tctctaa	1977

<210> 54

<211> 658

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(31)

<221> BINDING

<222> (32)...(124)

<223> Carbohydrate binding module

<221> BINDING

<222> (180)...(303)

<223> Carbohydrate binding module

<221> DOMAIN

<222> (304)...(658)

<223> Catalytic domain

<400> 54

Met	Asn	Asn	Ser	Thr	Lys	Lys	Met	Ile	Arg	Pro	Leu	Lys	Ala	Ser	Phe
1							5			10			15		
Ala	Leu	Gly	Ala	Leu	Ala	Leu	Ala	Ile	Ala	Ser	Pro	Ser	Trp	Ala	Ala
							20			25			30		
Cys	Ser	Tyr	Ser	Val	Thr	Asn	Asn	Trp	Gly	Ser	Gly	Phe	Thr	Gly	Glu
							35			40			45		
Ile	Lys	Val	Thr	Asn	Asp	Thr	Thr	Ser	Thr	Val	Asn	Asn	Trp	Ser	Val
							50			55			60		
Ser	Trp	Gln	Glu	Ser	Gly	Val	Thr	Val	Thr	Asn	Ala	Trp	Asn	Ala	Thr
							65			70			75		80
Leu	Ser	Gly	Ser	Asn	Pro	Tyr	Thr	Ala	Thr	Ser	Leu	Gly	Trp	Asn	Gly
							85			90			95		
Thr	Leu	Ala	Pro	Lys	Ala	Ser	Ala	Ser	Phe	Gly	Phe	Gln	Ala	Asn	Gly
							100			105			110		
Thr	Ala	Gly	Ala	Pro	Lys	Val	Asn	Gly	Thr	Leu	Cys	Gly	Thr	Ser	Thr

115	120	125
Ser Ser Thr Gly Thr Ser Ser Val Ala Pro Ser Ser Val Ala Ser Ser		
130	135	140
Val Ala Val Ser Ser Ser Lys Ser Ser Ser Ser Val Ala Thr Ile Ser		
145	150	155
Ser Ser Lys Ser Ser Ser Val Pro Thr Val Ser Ser Phe Thr Ile		
165	170	175
Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile Ala Thr Glu		
180	185	190
Ser Thr Asn Thr Gly Tyr Thr Gly Asn Gly Tyr Thr Asn Thr Thr Asn		
195	200	205
Ala Gln Gly Ala Ala Ile Glu Trp Ala Ile Asn Ala Pro Asn Ser Ser		
210	215	220
Arg Tyr Thr Leu Thr Phe Arg Tyr Ala Asn Ala Gly Thr Ala Asn Arg		
225	230	235
Asn Gly Ser Leu Leu Ile Asn Asp Gly Ser Asn Gly Asn Tyr Thr Val		
245	250	255
Gln Leu Pro Ser Thr Gly Ala Trp Ala Thr Trp Gln Thr Val Ser Val		
260	265	270
Glu Val Asp Leu Val Gln Gly Asn Asn Ile Leu Lys Leu Ala Ser Leu		
275	280	285
Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile Glu Gly Ala		
290	295	300
Gln Ala Lys Ala Gly Val Cys Ser Thr Thr Val Ser Ser Ser Ser Ser		
305	310	315
Ser Ile Lys Ser Ser Ser Ser Ser Ser Ser Thr Ala Ala		
325	330	335
Val Lys Thr Leu Thr Leu Asp Gly Asn Pro Ala Ala Asn Trp Phe Asn		
340	345	350
Lys Ser Arg Thr Lys Trp Asn Val Ser Arg Ala Asp Ile Val Leu Ser		
355	360	365
Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn Ser		
370	375	380
Val Gly Ser Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn Gly		
385	390	395
Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Val Tyr Lys Asn Gly		
405	410	415
Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe Ile		
420	425	430
Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro Leu		
435	440	445
Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn Asp Asn Gly Met Ala		
450	455	460
Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn Lys Arg Ala Pro Phe		
465	470	475
Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ser Lys Phe Lys Thr Ala		
485	490	495
Val Thr Lys Gly Val Asp Tyr Ile Leu Lys Ala Gln Trp Lys Gln Asn		
500	505	510
Gly Lys Leu Thr Val Trp Cys Ala Gln His Gly Ala Asn Asp Tyr Gln		
515	520	525
Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Ser Glu		
530	535	540
Ser Val Gly Val Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Thr Gln		
545	550	555
Ile Glu Ala Ala Val Arg Ala Gly Val Ala Trp Phe Asn Ser Pro Ser		
565	570	575
Thr Tyr Leu Asn Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr Asn		
580	585	590

Pro Ile Val Pro Lys Ser Gly Ser Lys Met Trp Tyr Arg Phe Tyr Asp
 595 600 605
 Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys Phe
 610 615 620
 Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser Trp
 625 630 635 640
 Gly Gly Asp Tyr Gly Ser Ser Ile Ile Ser Phe Ala Gln Lys Val Gly
 645 650 655
 Tyr Leu

<210> 55

<211> 1125

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 55

gtggccctag gtaataacgg	cgccagcttg	agttgcgtcc	aatatattgt	gattgtgaaa	60
ggacccgggt	gacctcgacc	gccggtaaa	ccggccgtcc	aggcccccgt	120
tggagcgcac	gcctagcca	gcccggcggaa	tggacggaa	gtgacgaagc	180
gcggacaaacg	tcctcctcta	ccagcgcac	accggcgggt	ggtcgaaagg	240
gcccggccca	tcccggaaaca	caggaagtcc	ttttcctca	ccgagaagg	300
gactcgaacca	tcgacaacgg	tggcaccgtg	accagctca	agtatctcgc	360
aaggcgaacca	ggctgaaacg	gttcaaggag	ggcttcctca	aaggctcga	420
gcccggccagt	acccgaacgg	cgctggccc	cagtattatc	ctaacattcga	480
gccaacatca	cttataacga	caatgccat	gtgaacgtgc	tcaccctcct	540
gccaaaaagg	ccccggagta	cgacttcgtc	gaccggcgc	gcccggagaa	600
gcccgtggcga	aagggatcga	ctgcacatc	aagaccaga	tccgtgtcaa	660
accgcctgg	gcccggcagca	tgaccccaag	acgctggcgc	ccgcgcggc	720
gagctttagt	ccatcagcgg	tttcgagagc	gtcgggatcg	tccgggttctt	780
gagaatccga	gcccgaaggt	catcgaggcg	gtagaggccg	ccgtgaaatg	840
gtcaagctta	ccgggatcaa	gttggtcgag	aaaccggacc	cgcccttcc	900
gaccgcgtgg	tggtcaaga	ccccaaacgcg	ccgcccattc	gggccccgtt	960
ggcaccaacc	gtcccttctt	ctgcggccgc	gatggtatca	ctacgagatc	1020
atcaacacg	aacgggggt	cgttactcc	tggtacacca	atgccccggc	1080
gagaaggagt	atccgctctg	gcccccaaa	caccctacca	atgaa	1125

<210> 56

<211> 374

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(374)

<223> Catalytic domain

<400> 56

Met Val Leu Gly Asn Asn Gly	Gly Ser	Leu Ser Cys Val Gln Tyr Ile		
1	5	10	15	
Val Ile Val Lys Gly Pro Gly	Gly Pro Arg Pro Pro Val Lys Pro Ala			
20	25	30		
Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Cys Leu Val Gln Arg				
35	40	45		

Pro Glu Trp Tyr Gly Ser Asp Glu Ala Ile Arg Ile Ala Asp Asn Val
 50 55 60
 Leu Leu Tyr Gln Arg Asn Thr Gly Gly Trp Pro Lys Asp Ile Asp Met
 65 70 75 80
 Ala Glu Pro Ile Pro Glu His Arg Lys Ser Phe Phe Leu Thr Glu Lys
 85 90 95
 Glu Arg Thr Asp Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Gln
 100 105 110
 Leu Lys Tyr Leu Ala Arg Val Tyr Lys Ala Thr Arg Leu Glu Arg Phe
 115 120 125
 Lys Glu Gly Phe Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
 130 135 140
 Pro Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Asn Leu Arg Gly Tyr Tyr
 145 150 155 160
 Ala Asn Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Leu
 165 170 175
 Leu Gln Ser Ile Ala Lys Lys Ala Pro Glu Tyr Asp Phe Val Asp Pro
 180 185 190
 Ala Arg Arg Glu Lys Ala Ala Arg Ala Val Ala Lys Gly Ile Asp Cys
 195 200 205
 Ile Leu Lys Thr Gln Ile Arg Val Asn Gly Lys Leu Thr Ala Trp Cys
 210 215 220
 Ala Gln His Asp Pro Lys Thr Leu Ala Pro Ala Pro Ala Arg Ser Tyr
 225 230 235 240
 Glu Leu Glu Ser Ile Ser Gly Phe Glu Ser Val Gly Ile Val Arg Phe
 245 250 255
 Leu Met Ser Leu Glu Asn Pro Ser Pro Lys Val Ile Glu Ala Val Glu
 260 265 270
 Ala Ala Val Lys Trp Phe Glu Glu Val Lys Leu Thr Gly Ile Lys Val
 275 280 285
 Val Glu Lys Pro Asp Pro Ser Leu Pro Gly Gly Tyr Asp Arg Val Val
 290 295 300
 Val Glu Asp Pro Asn Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile
 305 310 315 320
 Gly Thr Asn Arg Pro Phe Phe Cys Gly Arg Asp Gly Ile Lys Lys Tyr
 325 330 335
 Ser Leu Ala Glu Ile Glu His Glu Arg Arg Val Gly Tyr Ser Trp Tyr
 340 345 350
 Thr Asn Ala Pro Ala Tyr Leu Ile Glu Lys Glu Tyr Pro Leu Trp Arg
 355 360 365
 Ala Lys His Pro Thr Lys
 370

<210> 57

<211> 1170

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 57

atggacaaac	gcgtcaaatg	gattcatca	gcttcaaaag	aagaagcaaa	gcagttcgag	60
ccggaaaatt	tcctcaaagg	caaagacggc	tggatccga	aaaaggcgga	tgaccgctgg	120
ctcgaaaaaa	caaaacctga	ctggcagctc	gttacgtgga	acgacgcgtt	acgccaggcg	180
ccgctctgg	atcaaaccga	tgaagcggcg	cgcattgccg	accaggtat	tttgtaccag	240
aaagacaacg	gcccgtgg	aaaaaatctc	gatatgacgg	cgatgctcac	gcaagccgaa	300
cgcggaaa	tcgc	aaaaatcgaa	acgtcgaaa	cgacgatcga	caaccgcacg	360
acccatcacgc	aagtgcctt	tctgc	ccaaa	gtcattacgg	gcagcttgca	420

ccggccgacca	atttccgaa	acataaggaa	gctttttca	agggcttgg	ttacctgctc	480
gcgtcgagt	acgaatcggg	cggtttccg	cagttttatc	cgctcaaaaa	agtttattac	540
acgcacatca	cgttcaacga	cgatgcgt	attggcg	tgaagggtt	gcgcgaaatc	600
gccaaggaaa	aggaagacta	tcttttgg	gacgaagaac	gccgcctgaa	agcgaaaaaa	660
tcggcgaaa	aagcgctg	ctgttctg	aaattgcagg	ttgaagtcgg	cgccaaaaaa	720
acggtttgg	cgcgca	tgacgaaaac	actttaaac	ccgcagccgc	gcgaaagttt	780
gaaccgg	tttaacggc	gggcgaatcg	gtcggcatcg	tccggttt	aatgtacgt	840
tcaaagccc	accaggcgac	gattgacg	attgaatctg	ccattcagtg	gtatcgcg	900
aacaaaatcg	aaggcattcg	atgggtgcgc	gaaaacggcg	aaaaccgcgt	cgtcaaggac	960
aaaaacgcgc	cgccgattt	ggcgcgg	tacgaaatcg	aaacgatgaa	gccgattt	1020
atcgggcgc	acgcatcat	tcgttacgac	gtgtctgaaa	tcgaagccg	gcggcgaac	1080
ggctacgcgt	ggtacgtctc	ggagccg	gagctgctt	aaaaagatta	ccgaaatgg	1140
ctggaaaaaa	ttaaaaaaatc	agtaaaagtaa				1170

<210> 58
<211> 389
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(389)
<223> Catalytic domain

<400> 58
Met Asp Lys Arg Val Lys Trp Ile His Gln Leu Ser Lys Glu Glu Ala
1 5 10 15
Lys Gln Phe Glu Pro Glu Asn Phe Leu Lys Gly Lys Asp Gly Trp Asn
20 25 30
Pro Lys Lys Ala Asp Asp Arg Trp Leu Glu Lys Thr Lys Pro Asp Trp
35 40 45
Gln Leu Val Thr Trp Asn Asp Ala Leu Arg Gln Ala Pro Leu Trp Tyr
50 55 60
Gln Thr Asp Glu Ala Ala Arg Ile Ala Asp Gln Val Ile Leu Tyr Gln
65 70 75 80
Lys Asp Asn Gly Gly Trp Glu Lys Asn Leu Asp Met Thr Ala Met Leu
85 90 95
Thr Gln Ala Glu Arg Glu Lys Leu Ala Lys Glu Lys Ser Asn Thr Ser
100 105 110
Glu Thr Thr Ile Asp Asn Arg Thr Thr Tyr Thr Gln Val Ala Phe Leu
115 120 125
Ala Lys Val Ile Thr Gly Ser Leu Gln Lys Thr Thr Pro Pro Thr Asn
130 135 140
Phe Pro Lys His Lys Glu Ala Phe Phe Lys Gly Leu Asp Tyr Leu Leu
145 150 155 160
Ala Ser Gln Tyr Glu Ser Gly Gly Phe Pro Gln Phe Tyr Pro Leu Lys
165 170 175
Lys Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asp Ala Met Ile Gly
180 185 190
Val Leu Lys Val Leu Arg Glu Ile Ala Lys Lys Glu Asp Tyr Leu
195 200 205
Phe Val Asp Glu Glu Arg Arg Leu Lys Ala Glu Lys Ser Val Glu Lys
210 215 220
Ala Leu Pro Leu Ile Leu Lys Leu Gln Val Glu Val Gly Gly Lys Lys
225 230 235 240
Thr Val Trp Ala Ala Gln Tyr Asp Glu Asn Thr Phe Lys Pro Ala Ala
245 250 255

Ala Arg Lys Phe Glu Pro Val Ser Leu Thr Ala Gly Glu Ser Val Gly
 260 265 270
 Ile Val Arg Phe Leu Met Tyr Asp Ser Lys Pro Asp Gln Ala Thr Ile
 275 280 285
 Asp Ala Ile Glu Ser Ala Ile Gln Trp Tyr Arg Ala Asn Lys Ile Glu
 290 295 300
 Gly Ile Arg Trp Val Arg Glu Asn Gly Glu Asn Arg Val Val Lys Asp
 305 310 315 320
 Lys Asn Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile Glu Thr Met
 325 330 335
 Lys Pro Ile Phe Ile Gly Arg Asp Ala Ile Ile Arg Tyr Asp Val Ser
 340 345 350
 Glu Ile Glu Ala Glu Arg Arg Asn Gly Tyr Ala Trp Tyr Val Ser Glu
 355 360 365
 Pro Asn Glu Leu Leu Glu Lys Asp Tyr Pro Lys Trp Leu Glu Lys Ile
 370 375 380
 Lys Lys Ser Val Lys
 385

<210> 59

<211> 1080

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 59
 atgagaatcc ggtccttcc aatcgcttc ggcctgattt gcagtctggc gctaagggtg 60
 cctgcgcaag cgcaggcac cgtgcgtgg gcggacgtcc tgaaccagcc cgccgcctgg 120
 tatggcaccg atgaagcccg tcgaattgcc gaccacgtgc tcgagcatca acgagcggaa 180
 ggcggatggc caaagaacac ggacatgacc gcagcgcggc atccggcgtt gtcacacagcc 240
 ggcgcagtga agccagactc gacgatcgat aacggcgca cctgcactga aatgcgcgtc 300
 ctcgcgcgcg tctaccgttc atcaccgcgat ccccggttgc gcgatgcgt gctcaagggt 360
 ctcgactatc tggatggcgcg gcagttatgcc aacggcggtt ggccgcgtt ctaccgcgc 420
 cggcaggact attcgcccta tatcacgttc aacgacaacg cgatgtatcaa tggatgtacg 480
 ctgcgttcag acgtcgctgc cggaaatggc gactggcgat ttgcgtatgc cagccggcgc 540
 gagaaaaagcc ggacggctgt agagaaggcc gtagaaatgtca tcctgcgcgc gcagggtgaga 600
 gttgacggcc ggctgaccgc gtggatggcgc caacacgacg aggtgacact cgagccgcgc 660
 aaggccgcgc cctacgaaca tccgtcgctg agcggacagg agacgggtgg gatcatccgg 720
 tttctcatga cccgcgataa accggatcg agagtcgtcg atgcaatcg ggcgtcagtg 780
 gcatggctga agggcggtgca gctcaaaggga cttcgctgc accagcgccg cgatccctcg 840
 ctgcggagg ggcgtgacgt ggtgaccgtc gctgaccgtt cggcgccgc gctctggcg 900
 cgcttctacg aaatcgccgc caatcgcccg atcttcgtcg gacgacgacgg cgtgatccga 960
 tactcgctgg cagagatcgaa gcacgaacgc cggataagggt acgcctggct cggaaacctgg 1020
 cccgcgaaacg tgctcgatac cgaataccca tcctggcgac ggactcaaca aaggccgtga 1080

<210> 60

<211> 359

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(24)

<221> DOMAIN

<222> (25)...(359)
 <223> Catalytic domain

<400> 60
 Met Arg Ile Arg Ser Ser Ser Ile Ala Phe Gly Leu Ile Cys Ser Leu
 1 5 10 15
 Ala Leu Arg Val Pro Ala Gln Ala Gln Val Thr Val Arg Trp Ala Asp
 20 25 30
 Val Leu Asn Gln Pro Ala Ala Trp Tyr Gly Thr Asp Glu Ala Arg Arg
 35 40 45
 Ile Ala Asp His Val Leu Glu His Gln Arg Ala Glu Gly Gly Trp Pro
 50 55 60
 Lys Asn Thr Asp Met Thr Ala Ala Pro Asp Pro Ala Val Leu Thr Ala
 65 70 75 80
 Ala Arg Val Lys Pro Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr
 85 90 95
 Glu Met Arg Val Leu Ala Arg Val Tyr Arg Ser Ser Pro Asp Pro Arg
 100 105 110
 Tyr Arg Asp Ala Leu Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln
 115 120 125
 Tyr Ala Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Arg Gln Asp Tyr
 130 135 140
 Ser Arg Tyr Ile Thr Phe Asn Asp Asn Ala Met Ile Asn Val Val Thr
 145 150 155 160
 Leu Leu Ser Asp Val Ala Ala Gly Asn Gly Asp Trp Ala Phe Ala Asp
 165 170 175
 Ala Ser Arg Arg Glu Lys Ser Arg Thr Ala Val Glu Lys Ala Val Glu
 180 185 190
 Val Ile Leu Arg Ala Gln Val Arg Val Asp Gly Arg Leu Thr Ala Trp
 195 200 205
 Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Arg Lys Ala Arg Ala
 210 215 220
 Tyr Glu His Pro Ser Leu Ser Gly Gln Glu Thr Val Gly Ile Ile Arg
 225 230 235 240
 Phe Leu Met Thr Arg Asp Lys Pro Asp Gln Arg Val Val Asp Ala Ile
 245 250 255
 Glu Ala Ser Val Ala Trp Leu Lys Ala Val Gln Leu Lys Gly Leu Arg
 260 265 270
 Val Asp Gln Arg Arg Asp Pro Ser Leu Pro Glu Gly Arg Asp Val Val
 275 280 285
 Thr Val Ala Asp Pro Ser Ala Pro Pro Leu Trp Ala Arg Phe Tyr Glu
 290 295 300
 Ile Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Gly Val Ile Arg
 305 310 315 320
 Tyr Ser Leu Ala Glu Ile Glu His Glu Arg Arg Ile Gly Tyr Ala Trp
 325 330 335
 Leu Gly Thr Trp Pro Ala Lys Leu Leu Asp Thr Glu Tyr Pro Ser Trp
 340 345 350
 Arg Arg Thr Gln Gln Arg Pro
 355

<210> 61
 <211> 1224
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 61

```

gtgaaattac cagtaaccgg cgcatggca acctggcaaa ccgcaactgt taaaattgat      60
tttgtcaag gtaacaacct gtaaaaactt tctgcatca cggctgatgg tttggcaat      120
atcgattcgt tgaaaattga cggcgcacaa accaaagccg gcgtgtcag cactgtggca      180
agcagcagct cttcatccgt tgcttcatcg attaatcaa gctccagtc atccctttcc      240
agttcaacga cgacggtaaa aacattaaca ctggatggca accccgcagc aaactggtt      300
aacaatcca gaaccaaattg gaataccagc agagccgatg ttgtacttc ctatcaacaa      360
tccaacggcg gctggccaaa aatctcgat tacaattcag taagcgcagg taatggcg      420
agcgatagcg gcaccatcgta taacggtgca accattactg aatggttt tctcgcgaa      480
gttacaaaaa atggcaacaa caccaagtat cgcgatgcgg tgcgcagagc cgcaatttt      540
attgtcagct cgcaatacag cactggtgca ttaccacaat tttatccatt gaaaggcg      600
tatgcagacc acgccaccc taaacgataac ggcattggcat atgcattaaac ggtattggat      660
tttgcagtca acaaacgcgc cccatttgat actgatgtt tctccgattc tgatcgcg      720
aaattcaaaa ccgctgtgc caaagggtgt gattacatt taaaagcga gtggaaacaa      780
aacggaaaaat taaccgtgt gttgcacaa catggtgcta ccgattatca accgaaaaaa      840
gcccgcgcct atgaatttggaa atcaactgat ggcagcgaat ctgttgggt actcgcttc      900
ttgatgaccc aaccgcaaac cgccacaaattt gaagccgctg taaaagccgg ttagcctgg      960
ttcaatagcc ccaacacgtt tttgaacaat tacacttacg actcttcaaa agcgtcaact      1020
aatccaatag ttgccaagtc tggaaagcaaa atgtgttacg gttttacga tttaaatacc      1080
aatcgtggct tcttcagtga tccgcgatggc agcaattct atgacatcac ccagatgtca      1140
gaagagcgctc gcactggata tagctgggt ggtgattacg gcacgtcgat tatttccttc      1200
gcgcacaaag tggatatact gtaa                                         1224

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<210> 62

<211> 407

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (0)...(407)

<223> Catalytic domain

<400> 62

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Met Glu Leu Pro Val Thr Gly Ala Trp Ala Thr Trp Gln Thr Ala Thr      15
      5          10          15
Val Glu Ile Asp Leu Val Gln Gly Asn Asn Leu Leu Lys Leu Ser Ala      30
      20          25          30
Ile Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile Asp Gly      45
      35          40          45
Ala Gln Thr Lys Ala Gly Val Cys Ser Thr Val Ala Ser Ser Ser Ser      60
      50          55          60
Ser Ser Val Ala Ser Ser Ile Lys Ser Ser Ser Ser Ser Ser Ser Ser      80
      65          70          75          80
Ser Ser Thr Thr Val Lys Thr Leu Thr Leu Asp Gly Asn Pro Ala      95
      85          90          95
Ala Asn Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Thr Ser Arg Ala      110
      100         105         110
Asp Val Val Leu Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn      125
      115         120         125
Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly      140
      130         135         140
Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu      160
      145         150         155         160
Val Tyr Lys Asn Gly Asn Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg      175
      165         170         175
Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro

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180	185	190
Gln Phe Tyr Pro Leu Lys Gly	Gly Tyr Ala Asp His	Ala Thr Phe Asn
195	200	205
Asp Asn Gly Met Ala Tyr Ala	Leu Thr Val Leu Asp	Phe Ala Val Asn
210	215	220
Lys Arg Ala Pro Phe Asp	Thr Asp Val Phe	Ser Asp Ser Asp Arg Ala
225	230	235
Lys Phe Lys Thr Ala Val Ala	Lys Gly Val Asp	Tyr Ile Leu Lys Ala
245	250	255
Gln Trp Lys Gln Asn Gly	Lys Leu Thr Val Trp Cys	Ala Gln His Gly
260	265	270
Ala Thr Asp Tyr Gln Pro Lys	Lys Ala Arg Ala	Tyr Glu Leu Glu Ser
275	280	285
Leu Ser Gly Ser Glu Ser Val	Gly Val Leu Ala	Phe Leu Met Thr Gln
290	295	300
Pro Gln Thr Ala Gln Ile	Glu Ala Ala Val	Lys Ala Gly Val Ala Trp
305	310	315
Phe Asn Ser Pro Asn Thr Tyr	Leu Asn Asn Tyr	Thr Tyr Asp Ser Ser
325	330	335
Lys Ala Ser Thr Asn Pro Ile	Val Ala Lys Ser	Gly Ser Lys Met Trp
340	345	350
Tyr Arg Phe Tyr Asp Leu Asn	Thr Asn Arg Gly	Phe Phe Ser Asp Arg
355	360	365
Asp Gly Ser Lys Phe Tyr Asp	Ile Thr Gln Met	Ser Glu Glu Arg Arg
370	375	380
Thr Gly Tyr Ser Trp Gly	Gly Asp Tyr Gly	Thr Ser Ile Ile Ser Phe
385	390	395
Ala Gln Lys Val Gly Tyr Leu		400
	405	

<210> 63

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 63	60	
atgttaagtt tcatcgccgt atcagtgttt cataattact	gtacaggca gactgcgtcc	60
acccaaaaatt cagtggccga aaagatgctt	cagtaccagt tgtcaaatgg	120
aaacacgttgg tagacaaaag	cgccctggccc	180
tgtcggtat tacagtcttc	cattaacgaa agagctccta	240
cagcagatca agaaaacaga	tattgtatcat gctacgctcg	300
gaaataactg aattgtatcaa	acaacagtcg gacaacccgg	360
ggatggaaagg ggattgcata	tatTTTATCG gctcaatatg	420
tactacccaa ataaattata	agaatggcg	480
ctatagagct gagataacat	atttccacaa	540
aatgcattac tagtgcTTA	acaacgatga	600
cccatatttg tgtcaaaagc	tgcgtatgatc	660
gcaaaaagca gttgaaaagg	ggctatcaat	720
gtataacctg tattggcata	cccataatttgc	780
acacaggtca tacaagacgg	tttgcgtatcaat	840
aaaaaggagt atttggctg	ccatggatgtt	900
ttacaacctg ctcaggcaag	ccatggatgtt	960
aaagtggatccat tgaggcacaag	ccatggatgtt	1020
tccatcggtt gctttctcat	ccatggatgtt	1023
gctacagccct gcaaccactg	ccatggatgtt	
catgcaatac aatgggtcga	ccatggatgtt	
acagcatgtat attgaagggtt	ccatggatgtt	
gatagggtga ctggaaaata	ccatggatgtt	
tcaacggcag cttgtcgctg	ccatggatgtt	
gcccgtttt ataatctcgaa	ccatggatgtt	
agacaaccgt ccattgtttg	ccatggatgtt	
aaataacaact ttgaggaggt	ccatggatgtt	
tgcaggaggag cgtaaaatg	ccatggatgtt	
ttcagaggaggag cgtaaaatg	ccatggatgtt	
tgcccgaaa agctgatcca	ccatggatgtt	
aaaggactat ccaaaatgga	ccatggatgtt	
aaaaacaata caaaattcaa	ccatggatgtt	
taa	ccatggatgtt	

<210> 64

<211> 340

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(16)

<221> DOMAIN

<222> (17)...(340)

<223> Catalytic domain

<400> 64

Met	Leu	Ser	Phe	Ile	Ala	Val	Ser	Val	Phe	His	Asn	Tyr	Cys	Thr	Gly
1										5	10			15	
Gln	Thr	Ala	Ser	Thr	Lys	Asn	Ser	Val	Ala	Glu	Lys	Met	Leu	Gln	Tyr
										20	25			30	
Gln	Leu	Ser	Asn	Gly	Ala	Trp	Pro	Lys	Gln	Leu	Val	Asp	Lys	Ser	Val
										35	40			45	
Val	Asp	Tyr	Ser	Leu	Pro	Leu	Thr	Lys	Glu	Leu	Leu	Gln	Gln	Ile	Lys
										50	55			60	
Lys	Thr	Asp	Ile	Asp	His	Ala	Thr	Leu	Asp	Asn	Ser	Ala	Thr	Thr	Arg
										65	70			75	80
Glu	Ile	Thr	Glu	Leu	Ile	Lys	Ala	Phe	Lys	Asp	Thr	Lys	Asn	Lys	Ala
										85	90			95	
Tyr	Leu	Thr	Ala	Ala	Glu	Lys	Gly	Ile	Ala	Tyr	Ile	Leu	Ser	Ala	Gln
										100	105			110	
Tyr	Glu	Asn	Gly	Gly	Phe	Pro	Gln	Tyr	Tyr	Pro	Asn	Lys	Leu	Tyr	Tyr
										115	120			125	
Arg	Ala	Glu	Ile	Thr	Tyr	Asn	Asp	Asp	Ala	Met	Ile	Asn	Ala	Leu	Leu
										130	135			140	
Val	Leu	Tyr	Lys	Val	Ala	Asn	Lys	Arg	Glu	Gly	Phe	Glu	Ala	Ile	Asn
										145	150			155	160
Pro	Ile	Phe	Val	Ser	Lys	Ala	Gln	Lys	Ala	Val	Glu	Lys	Gly	Ile	Thr
										165	170			175	
Cys	Ile	Leu	Lys	Thr	Gln	Val	Ile	Gln	Asp	Gly	Lys	Arg	Ser	Ile	Trp
										180	185			190	
Ala	Ala	Gln	Tyr	Asp	Gln	Asn	Thr	Leu	Gln	Pro	Ala	Gln	Ala	Arg	Lys
										195	200			205	
Phe	Glu	Pro	Ala	Ser	Leu	Ser	Thr	Ser	Glu	Ser	Val	Ser	Ile	Val	Arg
										210	215			220	
Phe	Leu	Met	Leu	Gln	Pro	Ala	Thr	Thr	Glu	Ile	Lys	Gln	Ala	Ile	Glu
										225	230			235	240
His	Ala	Ile	Gln	Trp	Phe	Glu	Gln	His	Asp	Ile	Glu	Gly	Tyr	Arg	Phe
										245	250			255	
Asp	Arg	Ile	Gln	Asp	Arg	Val	Thr	Gly	Lys	Tyr	Gln	Arg	Gln	Leu	Val
										260	265			270	
Ala	Asp	Arg	Thr	Ser	Thr	Ile	Trp	Ala	Arg	Phe	Tyr	Asn	Leu	Glu	Asp
										275	280			285	
Asn	Arg	Pro	Leu	Phe	Gly	Asp	Arg	Asp	Asn	Thr	Ile	Lys	Tyr	Asn	Phe
										290	295			300	
Glu	Glu	Val	Ser	Glu	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Phe	Gly	Asn
										305	310			315	320
Trp	Pro	Glu	Lys	Leu	Ile	Gln	Lys	Asp	Tyr	Pro	Lys	Trp	Lys	Lys	Gln
										325	330			335	
Tyr	Lys	Ile	Gln												
															340

<210> 65
<211> 1311
<212> DNA
<213> Bacteria

<400> 65

gtgaaccgac	gtacccgcct	gggagcggtc	gccgcgaccg	ccctcgccct	gacggtcacc	60
gccccccgcg	ccgggtgcccc	cgccgcgcgt	ccccacgccc	cgccacgccc	gtcgccgat	120
ccggctcgcg	ccacgcgtgcc	cgccggcgac	ggctggcggt	ccgaggggac	cggcacgacc	180
ggtggggccg	ccgcccggagc	ctccccgggtc	ttcacccgtcg	ccacctggga	ggagttccgg	240
gccgcgctcg	cggtgccccg	ctcccgagccc	aggatcgta	aggtggtggg	cacgctgaac	300
gccaccgcgc	ccggctgcgg	cgccctcga	gcccggggct	acgacttcgc	ccgctacctc	360
gccgactacg	accggggccgt	gtgggggtac	gagaaggagg	ttagcggccc	gcaggaggag	420
ctgcggccgg	cgtccgcgcac	cgcgcagggc	caggccatca	aggtcaaggt	gccggcgaac	480
accacgatcg	tcggggtcgg	caggcacgcg	gggatcacgg	gcccggcagct	ccaggtgcag	540
ggcgtcgaca	acgtcggt	ccgcaacctg	acgctggaga	gcccgcgtca	ctgcttcccg	600
cagtgggacc	cgaccgacgg	cgcgaccggg	gcgtgaaact	ccgagtgacga	cagcctcgtc	660
gtgtacggct	ccaccatgt	ctggatcgac	cacaacacct	tcaccgacgg	cgcccccacccg	720
gacagttcgc	tgccctcgta	ctacggcgag	gtctaccagc	agcacgacgg	cgaaactggac	780
gtcgtcgccc	gcccggacct	cgtcacggtc	tcgtgaaacg	ccttcaccga	ccacgacaag	840
accctgatga	tcggcaacag	cgacagcgcg	ggcgcaccgc	accggggcaa	gctgcgggtc	900
accctgcacc	acaacctgtt	cgagaacgtc	gtcgagcggg	cgcccccgggt	caggttcggg	960
caggtcgacg	cgtacaacaa	ccacttcgtc	gtgcccagtt	cgccctacgc	gtacagcctg	1020
ggcgtcgccc	aggagtccca	gtcttcgcg	gagaagaacg	cgttcacct	cgccgggggc	1080
gtgcccggcg	ggaagatcct	caagaagtgg	aaggacgcgc	cggtcaccac	cgtcgcaac	1140
tacgtgaacg	gcaggccgt	cgacctgctc	gccgtccaca	acacccagt	cccggaggag	1200
cagttgcggg	ccgacgcggg	ctggacccccc	gtcctgcgca	ccagggtcga	ccacccgagg	1260
gccgtccccg	cgctcgctga	ccaccgcgcg	ggcgccggcc	gctcctgctg	a	1311

<210> 66
<211> 436
<212> PRT
<213> Bacteria

<220>

<221> SIGNAL
<222> (1)...(28)

<221> DOMAIN
<222> (29)...(436)
<223> Catalytic domain

<400> 66

Met	Asn	Arg	Arg	Thr	Arg	Leu	Gly	Ala	Val	Ala	Ala	Thr	Ala	Leu	Ala
1				5				10				15			
Leu	Thr	Val	Thr	Ala	Pro	Ala	Ala	Gly	Ala	His	Ala	Ala	Ala	Pro	His
				20				25				30			
Ala	Ala	Pro	Arg	Pro	Val	Ala	Asp	Pro	Ala	Arg	Ala	Thr	Leu	Pro	Ala
			35				40				45				
Gly	Asp	Gly	Trp	Ala	Ser	Glu	Gly	Thr	Gly	Thr	Gly	Gly	Ala	Ala	
			50			55			60						
Ala	Glu	Ala	Ser	Arg	Val	Phe	Thr	Val	Ala	Thr	Trp	Glu	Glu	Phe	Arg
65					70				75					80	
Ala	Ala	Leu	Ala	Val	Pro	Gly	Ser	Glu	Pro	Arg	Ile	Val	Lys	Val	Val
				85				90					95		
Gly	Thr	Leu	Asn	Ala	Thr	Ala	Ala	Gly	Cys	Gly	Ala	Phe	Glu	Ala	Pro
				100				105				110			

Gly Tyr Asp Phe Ala Arg Tyr Leu Ala Asp Tyr Asp Pro Ala Val Trp
 115 120 125
 Gly Tyr Glu Lys Glu Val Ser Gly Pro Gln Glu Glu Leu Arg Ala Ala
 130 135 140
 Ser Ala Thr Ala Gln Gly Gln Ala Ile Lys Val Lys Val Pro Ala Asn
 145 150 155 160
 Thr Thr Ile Val Gly Val Gly Arg His Ala Gly Ile Thr Gly Gly Ser
 165 170 175
 Leu Gln Val Gln Gly Val Asp Asn Val Val Val Arg Asn Leu Thr Leu
 180 185 190
 Glu Ser Pro Leu Asp Cys Phe Pro Gln Trp Asp Pro Thr Asp Gly Ala
 195 200 205
 Thr Gly Ala Trp Asn Ser Glu Tyr Asp Ser Leu Val Val Tyr Gly Ser
 210 215 220
 Thr His Val Trp Ile Asp His Asn Thr Phe Thr Asp Gly Ala His Pro
 225 230 235 240
 Asp Ser Ser Leu Pro Ser Tyr Tyr Gly Glu Val Tyr Gln Gln His Asp
 245 250 255
 Gly Glu Leu Asp Val Val Arg Gly Ala Asp Leu Val Thr Val Ser Trp
 260 265 270
 Asn Ala Phe Thr Asp His Asp Lys Thr Leu Met Ile Gly Asn Ser Asp
 275 280 285
 Ser Ala Gly Ala Thr Asp Arg Gly Lys Leu Arg Val Thr Leu His His
 290 295 300
 Asn Leu Phe Glu Asn Val Val Glu Arg Ala Pro Arg Val Arg Phe Gly
 305 310 315 320
 Gln Val Asp Ala Tyr Asn Asn His Phe Val Val Pro Ser Ser Ala Tyr
 325 330 335
 Ala Tyr Ser Leu Gly Val Gly Gln Glu Ser Gln Leu Phe Ala Glu Lys
 340 345 350
 Asn Ala Phe Thr Leu Ala Gly Gly Val Pro Ala Gly Lys Ile Leu Lys
 355 360 365
 Lys Trp Lys Asp Ala Pro Val Thr Thr Val Gly Asn Tyr Val Asn Gly
 370 375 380
 Arg Pro Val Asp Leu Leu Ala Val His Asn Thr Gln Phe Pro Glu Glu
 385 390 395 400
 Gln Leu Arg Ala Asp Ala Gly Trp Thr Pro Val Leu Arg Thr Arg Val
 405 410 415
 Asp His Pro Arg Ala Val Pro Ala Leu Val Asp His Arg Ala Gly Ala
 420 425 430
 Gly Arg Ser Cys
 435

<210> 67
 <211> 1995
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 67

atggaaaaatt	caaaaaactgt	tttactgca	aaaaaaaaac	tcatgcactc	ttgcattgcc	60
gccgctatcg	gcttggcgat	aagttcaggt	gcttggtcag	cttgcactta	cactgtcacc	120
aataattggg	gttctgctt	caccgggtgaa	atcaaagtta	ccaacaacac	atcatcggt	180
gttaatgggtt	ggtctgtgtc	ttggcaggaa	tcaggccat	cagtccacaa	ctcatggAAC	240
gcaactctga	gcggatcaa	tccttatacg	gcagccgcct	taggttggaa	tgcaactctc	300
gcacccgggtg	cttctgccag	tttggctt	caagcaaatg	gcactgctag	cgcaccta	360
gtaatggca	ctttatgtgg	aacagctact	tcatcaacac	ctgcgtcattc	cagcagtgtt	420

gcgagttcggtt	ttaaatcaag	cgcacccgtt	tcgtccagca	gtaaatcatc	cagctcaatc	480
actgtgagta	gtagttctat	cgccagcagc	agcgcaccaa	gtgtttcttc	attacaatt	540
caggaagagc	aagctggctt	ctgtcggtt	gatggcattt	caacagaaaag	caccaacacc	600
ggctttaccg	gcaacccgcta	taccaatgca	aacaacgcac	aagggtcagc	gattgaatgg	660
gccccgtaaatg	caccgagcag	tggccgctac	acactcacat	tccgttttc	aaatggcgcc	720
actgcagcac	gcaatggttc	actgttaatt	aacggcggta	gcaatggtaa	ctacaccgtg	780
gatttaccac	taaccggcgc	atgggcgact	tggcaaacag	cgactgtaga	aatcgatttg	840
gtacaaggca	ccaacacgct	gaaactttct	gcattaaccg	cagatggctt	agctaataatc	900
gattcattaa	aaattgtatgg	caaccaaccc	aaagcaggca	cttgcagcaa	tacatcaagc	960
agtgttgcac	gcagttcttc	atccgttaaa	tccagttcaa	gttcttcatc	aagctcatcc	1020
accactgca	aaatgtgcac	tcttgatggc	aaccccgccg	caagttgggtt	caacaatcc	1080
agaacccaaat	ggaatagcag	tcgtgcggac	attgtgtgt	cttaccagca	agctaacggc	1140
ggctggccaa	aaaatctgga	ttacaactca	gtaagcgcag	gtaatgggtt	taggcacagc	1200
ggcactatcg	acaacccgccc	aaccatcag	gaaatggttt	atctcgcaaa	agtttataaa	1260
aacggggggca	atacaaaaata	tcgcgtatgca	gtacgtaaag	cggccaaactt	tattgtgagt	1320
tcgcaatacaca	gcacttgtgc	gttaccacaa	ttttaccat	tgaaagggtgg	ttatgcagat	1380
cacggccaccc	ttaacgataa	cggcatggct	tacgcattaa	cggtatttgg	ttttgcgggt	1440
aacaaacgtt	cggccgttga	taacgatgtt	ttttctgtat	cagaccgcgc	aaaattcaaa	1500
actgcccgtt	ccaaaggat	tgattacatt	ttgaaagccc	aatggaaaca	aatggaaaaa	1560
ctcaccgcatt	ggtgtgcgc	acacggagca	aacgactatc	aacccaaaagc	ggcgcgtgt	1620
tatgagttat	tatctttaag	cggcagcgaa	tccgttggca	tcatcgcttt	cctgtatgacc	1680
caaccacaaa	ctgcgcataat	cgaaggcagcg	gttaaagccg	gtgtaaaactt	gttcgcttagc	1740
cggccatatac	acttgctaa	ttacacctac	gactcgtcaa	aagcctctac	caatccgatt	1800
gtgtacaaat	ccggcagcag	aatgtgtat	cgcttctacg	atctgaacac	caatcgccga	1860
ttcttttagt	atcgcgatgg	cagcaaaattt	tatgacatca	ctcaaatgtc	tgaagaacgt	1920
cgcaccggct	acagctgggg	cggttcttac	ggtgaatcga	ttatcagctt	cgcgcacaaa	1980
gtgggttatac	tctaa					1995

<210> 68

<211> 664

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(32)

<221> BINDING

<222> (33)...(126)

<223> Carbohydrate binding module

<221> BINDING

<222> (184)...(307)

<223> Carbohydrate binding module

<221> DOMAIN

<222> (308)...(664)

<223> Catalytic domain

<400> 68

Met	Lys	Asn	Ser	Lys	Thr	Val	Phe	Thr	Ala	Gln	Lys	Lys	Leu	Met	His
1					5				10				15		
Ser	Cys	Ile	Ala	Ala	Ala	Ile	Gly	Leu	Ala	Ile	Ser	Ser	Gly	Ala	Trp
										20		25		30	
Ser	Ala	Cys	Thr	Tyr	Thr	Val	Thr	Asn	Asn	Trp	Gly	Ser	Gly	Phe	Thr
										35		40		45	
Gly	Glu	Ile	Lys	Val	Thr	Asn	Asn	Thr	Ser	Ser	Ala	Val	Asn	Gly	Trp

50	55	60
Ser Val Ser Trp Gln Glu Ser Gly Ala Ser Val Thr Asn Ser Trp Asn		
65	70	75
Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Ala Ala Leu Gly Trp		80
85	90	95
Asn Ala Thr Leu Ala Pro Gly Ala Ser Ala Ser Phe Gly Phe Gln Ala		
100	105	110
Asn Gly Thr Ala Ser Ala Pro Lys Val Asn Gly Thr Leu Cys Gly Thr		
115	120	125
Ala Thr Ser Ser Thr Pro Ala Ser Ser Ser Val Ala Ser Ser Val		
130	135	140
Lys Ser Ser Ala Pro Val Ser Ser Ser Lys Ser Ser Ser Ile		
145	150	155
160		
Thr Val Ser Ser Ser Ile Ala Ser Ser Ser Ala Pro Ser Val Ser		
165	170	175
Ser Leu Thr Ile Gln Glu Gln Ala Gly Phe Cys Arg Val Asp Gly		
180	185	190
Ile Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr		
195	200	205
Asn Ala Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Asn Ala		
210	215	220
Pro Ser Ser Gly Arg Tyr Thr Leu Thr Phe Arg Phe Ala Asn Gly Gly		
225	230	235
240		
Thr Ala Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly		
245	250	255
Asn Tyr Thr Val Asp Leu Pro Leu Thr Gly Ala Trp Ala Thr Trp Gln		
260	265	270
Thr Ala Thr Val Glu Ile Asp Leu Val Gln Gly Thr Asn Thr Leu Lys		
275	280	285
Leu Ser Ala Leu Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys		
290	295	300
Ile Asp Gly Asn Gln Pro Lys Ala Gly Thr Cys Ser Asn Thr Ser Ser		
305	310	315
320		
Ser Val Ala Ser Ser Ser Ser Val Lys Ser Ser Ser Ser Ser		
325	330	335
Ser Ser Ser Ser Thr Thr Ala Lys Met Leu Thr Leu Asp Gly Asn Pro		
340	345	350
Ala Ala Ser Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg		
355	360	365
Ala Asp Ile Val Leu Ser Tyr Gln Gln Ala Asn Gly Gly Trp Pro Lys		
370	375	380
Asn Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser		
385	390	395
400		
Gly Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala		
405	410	415
Glu Val Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg		
420	425	430
Lys Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu		
435	440	445
Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe		
450	455	460
Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val		
465	470	475
480		
Asn Lys Arg Ala Pro Phe Asp Asn Asp Val Phe Ser Asp Ala Asp Arg		
485	490	495
Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Ile Asp Tyr Ile Leu Lys		
500	505	510
Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His		
515	520	525

Gly Ala Asn Asp Tyr Gln Pro Lys Ala Ala Arg Ala Tyr Glu Leu Val
 530 535 540
 Ser Leu Ser Gly Ser Glu Ser Val Gly Ile Ile Ala Phe Leu Met Thr
 545 550 555 560
 Gln Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn
 565 570 575
 Trp Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser
 580 585 590
 Ser Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met
 595 600 605
 Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp
 610 615 620
 Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg
 625 630 635 640
 Arg Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser
 645 650 655
 Phe Ala Gln Lys Val Gly Tyr Leu
 660

<210> 69

<211> 1035

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 69
 atggcgcgtt tggccgggtg cgtgtgtgcc agcctggag gatggggccgc ggttctggcc 60
 gccgcggccgg gccccggattt gtcggccctg ctcgcgcac cggaccctt gtttcgcagt 120
 ccggcggggc aacaggcggt gacgaacgtt ttgtctggc agagcgcgac aggcgcctgg 180
 ccggaaaaacc tggacaccac cccgcgagccg cgtcgccagg attccgcccc gcccggaggc 240
 actttcgaca acggcgcac caccggcgag ttgcgtttc tggcgccggc gtttgcggcc 300
 accggcgatc cgcgctgcga agccgcgggt ctccggggc tggacggcat cctcgcggcc 360
 cagcttccca gggcgcgctg gccgcagtgt catcctccgc gcgcgcctta tcagcgcac 420
 atcaccttca acgacggtgt catggtgccg atcctggagc tgctgcgcga gatagaccgc 480
 gcgccggagt ttcgcgtgggt ggacgaggcg cggcgcgcgc gggtgccgc ggccttact 540
 cgcgggctgg agtgcctcct ggcgcgtccag gtggcgtcg agggcagact caccgtgtgg 600
 tggcccccac atgacgcgga gaactttcaa ccgcgaccgg cacgcgccta cgaactggaa 660
 tcgcctcagcg gcgcggaaag cgcggcgcgc ctgggttcc tcatgagct ggagccgcca 720
 accccggaga tcgcgcgcgc ggtcgaggcc ggggcggcct ggttttcggc ggtaaagctt 780
 gaagggttcc gtctcgaaacg aacggccgac gacgcgcggg tggtggaaaga gccggggcg 840
 cccgcgtct gggcgccgtt ctacgagatc gggaccaatc gccccatct tgccggcgc 900
 gacggtgtca agaagtaacgc cctgagcgag atcgagcggg aacgcccgggt cggctatgcg 960
 tggtaacggcg cctgggggtga accggtcgccc cggcattatg cccagtgccg ggagcggtac 1020
 gggacgcaga aatga 1035

<210> 70

<211> 344

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(22)

<221> DOMAIN

<222> (23)...(344)

<223> Catalytic domain

<400> 70

Met Ala Arg Leu Phe Arg Cys Val Cys Ala Ser Leu Gly Gly Trp Ala
 1 5 10 15
 Ala Val Leu Ala Ala Ala Gly Pro Asp Trp Ser Arg Leu Leu Ala
 20 25 30
 Gln Pro Asp Pro Trp Phe Arg Ser Pro Ala Gly Gln Gln Ala Val Thr
 35 40 45
 Asn Val Leu Ser Trp Gln Ser Ala Thr Gly Ala Trp Pro Lys Asn Leu
 50 55 60
 Asp Thr Thr Arg Glu Pro Arg Arg Gln Asp Ser Ala Pro Pro Glu Gly
 65 70 75 80
 Thr Phe Asp Asn Gly Ala Thr Thr Gly Glu Leu Arg Phe Leu Ala Arg
 85 90 95
 Ala Phe Ala Ala Thr Gly Asp Pro Arg Cys Glu Ala Ala Val Leu Arg
 100 105 110
 Gly Leu Asp Gly Ile Leu Ala Ala Gln Leu Pro Ser Gly Gly Trp Pro
 115 120 125
 Gln Cys His Pro Pro Arg Ala Pro Tyr Gln Arg His Ile Thr Phe Asn
 130 135 140
 Asp Gly Val Met Val Arg Ile Leu Glu Leu Leu Arg Glu Ile Asp Arg
 145 150 155 160
 Ala Pro Glu Phe Arg Trp Val Asp Glu Ala Arg Arg Ala Arg Val Arg
 165 170 175
 Ala Ala Phe Thr Arg Gly Leu Glu Cys Leu Leu Arg Cys Gln Val Val
 180 185 190
 Val Glu Gly Arg Leu Thr Val Trp Cys Ala Gln His Asp Ala Glu Asn
 195 200 205
 Phe Gln Pro Arg Pro Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly
 210 215 220
 Ala Glu Ser Ala Gly Ile Leu Val Phe Leu Met Ser Leu Glu Pro Pro
 225 230 235 240
 Thr Pro Glu Ile Ala Arg Ala Val Glu Ala Gly Ala Ala Trp Phe Ser
 245 250 255
 Ala Val Lys Leu Glu Gly Phe Arg Leu Glu Arg Thr Ala Asp Asp Ala
 260 265 270
 Arg Val Val Glu Glu Pro Gly Ala Pro Pro Leu Trp Ala Arg Phe Tyr
 275 280 285
 Glu Ile Gly Thr Asn Arg Pro Ile Phe Ala Gly Arg Asp Gly Val Lys
 290 295 300
 Lys Tyr Ala Leu Ser Glu Ile Glu Arg Glu Arg Arg Val Gly Tyr Ala
 305 310 315 320
 Trp Tyr Gly Ala Trp Gly Glu Pro Val Ala Arg His Tyr Ala Gln Trp
 325 330 335
 Arg Glu Arg Tyr Gly Thr Gln Lys
 340

<210> 71

<211> 1038

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 71

gtgactcgtg tcgcccttgc gatggggctt gttgcattgg ttccggcgct cgcttcagct

60

gggcccgtg	catatttgc	gaagccggac	gactggtcg	ccagtcccg	ggccaggc	120
atcgcccg	acgtactcgc	gcatcaggc	gatctcg	ggccggc	aaacatcg	180
acaacga	cgttcacccg	cgaccgg	acaatcaa	cggcc	taacacgc	240
acaaccg	agctccgtt	tctggcgc	atccaca	cgactcg	cgagaagt	300
cgccacc	tcgagaagg	gctcgatt	atcttga	cacaata	aaacggc	360
tggccg	cgt	cgcacccg	taccaccg	acatcac	caacgaca	420
gcacatgg	gtttatgg	gctcg	gaagtcg	cctcgaat	gtacgact	480
ctggacg	cccgcc	ggcctg	gccgctt	atcgccg	cgaatgc	540
ctgaagt	agatcaag	cgacagta	ctgacgg	ggtgcgc	gcacgacg	600
aaggac	ctccccc	ggcgcgg	tacgagct	tctca	cggctcg	660
tcggtcg	tcgtccgc	actcatg	ctcgatcg	caagccg	gtcgctcg	720
gcatcg	gcgcgtc	gtgg	tcggcga	tcaagg	caagg	780
gtcgag	acccgaag	tccggcgg	cggaa	gggtgg	ggatccaa	840
gcaccgc	tctggcgc	cttctacg	atcg	atcgtcc	900	
cgcgacgg	tcaagaag	cgcgtcg	gagatcg	ccgaacgg	aatggct	960
gcctgg	gac	ctggc	ctggaga	aataccagg	gtggaaaa	1020
aactgg	ggccgt	ga	gg	gg	aa	1038

<210> 72

<211> 345

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(20)

<221> DOMAIN

<222> (21)...(345)

<223> Catalytic domain

<400> 72

Met	Thr	Arg	Val	Ala	Leu	Ala	Met	Gly	Leu	Val	Ala	Trp	Val	Pro	Ala
1							5			10				15	
Leu	Ala	Ser	Ala	Gly	Pro	Ala	Ala	Tyr	Leu	Gln	Lys	Pro	Asp	Asp	Trp
							20			25				30	
Phe	Ala	Ser	Pro	Glu	Ala	Arg	Ala	Ile	Ala	Ala	Asn	Val	Leu	Ala	His
							35			40				45	
Gln	Ala	Asp	Leu	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Thr	Thr	Lys	Pro
							50			55				60	
Phe	Thr	Gly	Asp	Arg	Thr	Gln	Ile	Lys	Pro	Thr	Phe	Asp	Asn	Ser	Ala
							65			70				80	
Thr	Thr	Asp	Glu	Leu	Arg	Phe	Leu	Ala	Arg	Ile	His	Asn	Ala	Thr	Arg
							85			90				95	
Asp	Glu	Lys	Tyr	Arg	Thr	Ala	Phe	Glu	Lys	Gly	Leu	Asp	Tyr	Ile	Leu
							100			105				110	
Lys	Ala	Gln	Tyr	Ala	Asn	Gly	Gly	Trp	Pro	Gln	Ser	His	Pro	Pro	Gly
							115			120				125	
Thr	Gly	Tyr	His	Arg	His	Ile	Thr	Phe	Asn	Asp	Asn	Ala	Met	Val	Arg
							130			135				140	
Leu	Met	Glu	Leu	Val	Arg	Glu	Val	Ala	Thr	Ser	Asn	Arg	Tyr	Asp	Phe
							145			150				160	
Leu	Asp	Ala	Asp	Arg	Arg	Lys	Ala	Cys	Arg	Ala	Ala	Phe	Asp	Arg	Gly
							165			170				175	
Ile	Glu	Cys	Ile	Leu	Lys	Cys	Gln	Ile	Lys	Val	Asp	Ser	Lys	Leu	Thr
							180			185				190	
Ala	Trp	Cys	Ala	Gln	His	Asp	Glu	Lys	Asp	Leu	Ala	Pro	Arg	Pro	Ala

195	200	205	
Arg Thr Tyr Glu Leu Val Ser	Leu Ser Gly Ser	Glu Ser Val Gly Ile	
210	215	220	
Val Arg Leu Leu Met Ser	Leu Asp Arg Pro	Ser Pro Glu Val Ala Arg	
225	230	235	240
Ala Ile Asp Gly Ala Val	Ala Trp Phe Gln	Ser Ala Lys Leu Glu Gly	
245	250	255	
Thr Lys Val Val Val Glu	Arg Asp Pro Lys	Tyr Pro Gly Gly Arg Glu	
260	265	270	
Arg Val Val Val Lys Asp	Pro Lys Ala Pro Pro	Leu Trp Ala Arg Phe	
275	280	285	
Tyr Glu Ile Gly Thr Asn	Arg Pro Ile Phe Ser	Asp Arg Asp Gly Ile	
290	295	300	
Lys Lys Tyr Ala Leu	Ala Glu Ile Gly Pro	Glu Arg Arg Asn Gly Tyr	
305	310	315	320
Ala Trp Tyr Gly Thr Trp	Pro Arg Asp Leu	Leu Glu Lys Glu Tyr Pro	
325	330	335	
Gly Trp Lys Lys Lys	Leu Ala Arg Pro		
340	345		

<210> 73

<211> 1221

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 73				
atgctcacca aaacatcaact	acttattgc ttgctaggca	gttggatcat	cgaccattat	60
catgcggaca caccagcaag	caatgcaccc	acaaccaatg	catcaattcc	120
actgcgagcg	atgctgcgc	ctggaaaaat	tatctgcaca	180
gcagaccagg	cgcagctcaa	agccgagctg	aaaaaactcg	240
cctgagtaca	ccaaagaatt	tggtttga	gtgaagcagt	300
actgaaggta	aacgagtat	ggatattatc	catctgatg	360
tcaaaacgca	ctgacatgag	ctatcgttc	aaactccttc	420
aaaaattaca	caaagcgccg	cgcaaaacccg	gccaggcatt	480
caggcgcata	aagccactgg	cgataaacgc	cacaattat	540
tttatcatca	ccgctcaata	tcccaatggc	ggctgccac	600
aagtatcacg	atcacatcac	ttacaacgat	gccctgatgc	660
cacaagggtt	ccatggccaa	ggatgaattt	gcctttgtat	720
gcacaagcga	gcctcgaacg	cgccgctggac	ccaaggcgca	780
ggccaattaa	ctatatgggg	tgcgcagcac	gcaacaggcc	840
cgcgcctatg	aatgatttc	actcaccatgt	gatggatgt	900
atggatttc	aacagcccg	tttgcacat	cgatgttttgc	960
tatgagcaaa	ataaaattat	cgaaaaaacc	ttttatgaga	1020
gataaggatg	caccgccaat	ctggcgcgt	taggtacgaa	1080
tttggcggacc	gcgtgactc	tttgcattac	caaaccctg	1140
acgggttatg	cctggatcac	gatctggcaa	aggtatcgaa	1200
gctaaacaat	atccgcaata	aatcaggtat	agagcgccgc	1221

<210> 74

<211> 406

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(22)

<221> DOMAIN

<222> (23)...(406)

<223> Catalytic domain

<400> 74

Met	Leu	Thr	Lys	Thr	Ser	Leu	Leu	Ile	Ala	Leu	Leu	Gly	Ser	Cys	Cys			
1																		
														10	15			
Ile	Ala	Pro	Leu	His	Ala	Asp	Thr	Pro	Ala	Ser	Asn	Ala	Pro	Thr	Thr			
														20	25	30		
Asn	Ala	Ser	Ile	Pro	Leu	Gln	Gln	Thr	Ala	Ser	Asp	Ala	Ala	Ala	Trp			
															35	40	45	
Lys	Asn	Tyr	Leu	Ala	Lys	Ser	Asn	Glu	Leu	Arg	Lys	Ala	Asp	Gln	Ala			
															50	55	60	
Gln	Leu	Lys	Ala	Glu	Leu	Lys	Lys	Leu	Gly	Gln	Lys	Thr	Ala	Ser	Leu			
															65	70	75	80
Pro	Glu	Tyr	Thr	Lys	Glu	Phe	Gly	Glu	Val	Lys	Gln	Ser	Ser	Glu				
															85	90	95	
Trp	Phe	Lys	Ser	Thr	Glu	Gly	Lys	Arg	Val	Met	Asp	Ile	Ile	Leu	Ser			
															100	105	110	
Phe	Gln	Thr	Pro	Ser	Gly	Gly	Trp	Ser	Lys	Arg	Thr	Asp	Met	Ser	Lys			
															115	120	125	
Ala	Pro	Arg	Lys	Pro	Gly	Gln	Ala	Phe	Gly	Val	Glu	Lys	Asn	Tyr	Ile			
															130	135	140	
Pro	Thr	Phe	Asp	Asn	Gly	Ala	Thr	Ser	Thr	Gln	Leu	Met	Leu	Leu	Ala			
															145	150	155	160
Gln	Ala	His	Gln	Ala	Thr	Gly	Asp	Lys	Arg	Tyr	Ser	Asp	Ala	Phe	Ala			
															165	170	175	
Arg	Gly	Leu	Glu	Phe	Ile	Ile	Thr	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp			
															180	185	190	
Pro	Gln	Asn	Phe	Pro	Leu	Val	Gly	Lys	Tyr	His	Asp	His	Ile	Thr	Tyr			
															195	200	205	
Asn	Asp	Ala	Leu	Met	Arg	Asp	Leu	Met	Val	Val	Leu	His	Lys	Val	Ala			
															210	215	220	
Met	Ala	Lys	Asp	Glu	Phe	Ala	Phe	Val	Ser	Lys	Ala	Gln	Gln	Gln	Ala			
															225	230	235	240
Ala	Gln	Ala	Ser	Leu	Glu	Arg	Ala	Leu	Asp	Cys	Val	Leu	Lys	Thr	Gln			
															245	250	255	
Val	Met	Ala	Asn	Gly	Gln	Leu	Thr	Ile	Trp	Gly	Ala	Gln	His	Asp	Ala			
															260	265	270	
Lys	Thr	Leu	Lys	Pro	Ala	Lys	Ala	Arg	Ala	Tyr	Glu	Met	Ile	Ser	Leu			
															275	280	285	
Thr	Ser	Ser	Glu	Ser	Val	Trp	Met	Leu	Asp	Phe	Leu	Met	Asp	Leu	Gln			
															290	295	300	
Gln	Pro	Ser	Ala	Asp	Ile	Ile	Lys	Ser	Val	His	Ala	Ala	Ala	Ala	Trp			
															305	310	315	320
Tyr	Glu	Gln	Asn	Lys	Ile	Ile	Gly	Lys	Thr	Trp	Thr	Arg	Gly	Asp	Thr			
															325	330	335	
Val	Leu	Lys	Asp	Asp	Lys	Asp	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr			
															340	345	350	
Glu	Ile	Gly	Thr	Asn	Lys	Pro	Leu	Phe	Gly	Asp	Arg	Asp	Asp	Ser	Val			
															355	360	365	
His	Tyr	Asp	Leu	Ala	Lys	Val	Ser	Glu	Glu	Arg	Arg	Thr	Gly	Tyr	Ala			
															370	375	380	
Trp	Tyr	Thr	Thr	Ser	Pro	Asn	Gln	Val	Leu	Lys	Lys	Tyr	Ala	Arg	Trp			
															385	390	395	400
Ala	Lys	Gln	Tyr	Pro	Gln													

<210> 75
 <211> 1767
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 75

atgaccacaa	cccgccgcac	tatcctgaaa	gccgcgcgcca	gcgcggcg	gatgccagc	60
accggctggc	ccgccttggc	cgccgcacag	gccgcgaag	ccgcccaccc	gtggcccg	120
gcccagcaga	tcatcgaccg	tttcgcacaag	ccgctcagct	tcccgaacag	ggacttcccg	180
ataccggagt	tcggcgccaa	accctgcaag	ctggtcaaag	cccaggcgct	ggtcaagta	240
agagtcaaaag	gcaactcg	aacgcgcga	ccgcaagcgc	cgacgccta	cccgcaatc	300
aaaggccca	tcgcccgc	gagcaaggcc	ggaggaggc	cggtgctgat	cccgccggc	360
aactggta	tatcgtgctg	ctgtcaacg	tgcacgtgca	ccttgccaag	420	
ggcgcgcaag	tctacttcag	cgccaaacg	aaggacttcg	cccgcgacgg	480	
tgccgcgcca	acggcaagct	ggtgcgtcg	cgctggcaag	gcaacgattt	cctgaacttc	540
tcgcccattgg	tctacgcgc	cggccaaaag	aatatcgcca	ttaccggcga	agactggacc	600
agatcttga	acggccaggc	cggcgtggc	ttcgaagacg	gcagcggcaa	tggctgggt	660
ggcatgaacc	ccgcccggc	gccgcggc	agcaccacgc	accaggcg	agccaatccg	720
aacaacgccc	aggagccat	cgccagactg	cccacgcgc	acgcgaactg	gagcggcgc	780
gacaagtacc	tgccgctgct	gtccgaagcc	ggcgtgccc	ccgagcgc	cgtttcggt	840
ctggggcact	acctgcggcc	gtcgatggtc	gaattcgtcg	actgcggg	tgtgctgatg	900
cagggctacc	aggtcatcaa	cacgcgttc	tggattcata	acccggtaaa	ctcacgcaac	960
attcacttct	ccaaagtgc	catggaaagc	atcgcccc	attcgacgg	tttcgatccc	1020
gagtctcg	acaccatct	ggtgacgc	tgcctgttca	ataccggc	cgactgc	1080
gccatcaa	ccggcaagaa	ccgagactcg	caatacgcc	caacgcg	tatgtgg	1140
cagaactgca	tcatgaaccg	cggccacgc	ggcgttacgc	tggcagcga	aatggcggt	1200
ggcatcgagc	atatctacgc	gcagaaaatc	gaattccgca	acgcgttctg	ggaccacgac	1260
ccgctggca	ccgccccatcc	aatgaagacg	aacatgaacc	ggggcggt	ccttcgtcat	1320
ttctacgtgc	gcgacgtgc	gctgccaat	ggcgtgcgt	ccaagagcgg	cttctacaag	1380
acgctgccc	gatctccgct	ggcaggcaag	gtctccacca	ggggcggt	tgttatcact	1440
atcgactgc	attacgcgc	aatgacgc	acgcgtgc	tgcggccgc	gcaggtgtcg	1500
gacgtgcata	tctcgaacgt	ccgcgtc	aatgtaaaa	ggccgaa	ctcggtctcc	1560
tgttaccagg	ccatgggtct	gctcgcc	gtggcgcc	gttcaacgg	cgccctggc	1620
acggccatcc	tgccgatcac	aatgtcacc	gtcagcgatt	cgacttcg	cacggccgc	1680
aacagcgc	agccctgg	cgcgttcaac	gtcagggac	tcaagctgc	caacgtgc	1740
atcgatggca	aggagta	caa	cgtatga			1767

<210> 76
 <211> 588
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(34)

<221> DOMAIN
 <222> (110)...(555)
 <223> Catalytic domain

<400> 76
 Met Thr Thr Thr Arg Arg Thr Ile Leu Lys Ala Ala Ala Ser Ala Gly

1	5	10	15												
Ala	Ile	Ala	Ser	Thr	Gly	Trp	Pro	Ala	Leu	Ala	Ala	Gln	Ala	Ala	
		20				25						30			
Gln	Ala	Ala	Asp	Pro	Trp	Ala	Arg	Ala	Gln	Gln	Ile	Ile	Asp	Arg	Phe
												45			
		35				40									
Ala	Lys	Pro	Leu	Ser	Phe	Pro	Asn	Arg	Asp	Phe	Pro	Ile	Thr	Glu	Phe
												55		60	
Gly	Ala	Lys	Pro	Cys	Lys	Leu	Val	Lys	Ala	Gln	Gly	Leu	Val	Glu	Val
												75		80	
	65				70										
Arg	Val	Lys	Gly	Glu	Leu	Glu	Thr	Pro	Ala	Pro	Gln	Ala	Pro	Asp	Ala
												85		95	
Tyr	Pro	Ala	Ile	Lys	Ala	Ala	Ile	Ala	Ala	Ser	Lys	Ala	Gly	Gly	
												100		110	
Gly	Arg	Val	Leu	Ile	Pro	Ala	Gly	Asn	Trp	Tyr	Cys	Lys	Gly	Pro	Ile
												115		125	
Val	Leu	Leu	Ser	Asn	Val	His	Val	His	Leu	Ala	Lys	Gly	Ala	Gln	Val
												130		140	
Tyr	Phe	Ser	Ala	Asn	Ala	Lys	Asp	Phe	Ala	Arg	Asp	Gly	Asp	Tyr	Asp
												145		160	
Cys	Gly	Ala	Asn	Gly	Lys	Leu	Val	Leu	Ser	Arg	Trp	Gln	Gly	Asn	Asp
												165		175	
Cys	Leu	Asn	Phe	Ser	Pro	Met	Val	Tyr	Ala	Arg	Gly	Gln	Lys	Asn	Ile
												180		190	
Ala	Ile	Thr	Gly	Glu	Asp	Trp	Thr	Ser	Ile	Leu	Asn	Gly	Gln	Ala	Gly
												195		205	
Val	Ala	Phe	Glu	Asp	Gly	Ser	Gly	Asn	Gly	Trp	Trp	Gly	Met	Asn	Pro
												210		220	
Ala	Gly	Ala	Pro	Pro	Gly	Ser	Thr	Thr	His	Gln	Gly	Ala	Ala	Asn	Pro
												225		240	
Asn	Asn	Ala	Glu	Glu	Pro	Ile	Ala	Arg	Leu	Pro	Thr	Arg	His	Ala	Asn
												245		255	
Trp	Ser	Ala	Asp	Asp	Lys	Tyr	Leu	Pro	Leu	Leu	Ser	Glu	Ala	Gly	Val
												260		270	
Pro	Ala	Glu	Arg	Arg	Val	Phe	Gly	Leu	Gly	His	Tyr	Leu	Arg	Pro	Ser
												275		285	
Met	Val	Glu	Phe	Val	Asp	Cys	Gly	Asp	Val	Leu	Met	Gln	Gly	Tyr	Gln
												290		300	
Val	Ile	Asn	Thr	Pro	Phe	Trp	Ile	His	His	Pro	Val	Asn	Ser	Arg	Asn
												305		320	
Ile	His	Phe	Ser	Lys	Val	Arg	Met	Glu	Ser	Ile	Gly	Pro	Asn	Ser	Asp
												325		335	
Gly	Phe	Asp	Pro	Glu	Ser	Cys	Asp	Thr	Ile	Leu	Val	Asp	Gly	Cys	Leu
												340		350	
Phe	Asn	Thr	Gly	Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Lys	Asn	Arg
												355		365	
Asp	Ser	Gln	Tyr	Gly	Pro	Thr	Arg	Asn	Met	Val	Val	Gln	Asn	Cys	Ile
												370		380	
Met	Asn	Arg	Gly	His	Gly	Gly	Val	Thr	Leu	Gly	Ser	Glu	Met	Ala	Gly
												385		400	
Gly	Ile	Glu	His	Ile	Tyr	Ala	Gln	Lys	Ile	Glu	Phe	Arg	Asn	Ala	Phe
												405		415	
Trp	Asp	His	Asp	Pro	Leu	Gly	Thr	Ala	Ile	Arg	Met	Lys	Thr	Asn	Met
												420		430	
Asn	Arg	Gly	Gly	Tyr	Leu	Arg	His	Phe	Tyr	Val	Arg	Asp	Val	Thr	Leu
												435		445	
Pro	Asn	Gly	Val	Arg	Thr	Lys	Ser	Gly	Phe	Tyr	Lys	Thr	Leu	Pro	Gly
												450		460	
Ser	Pro	Leu	Ala	Gly	Lys	Val	Ser	Thr	Ser	Gly	Gly	Ala	Val	Ile	Thr
												465		475	
															480

Ile	Asp	Cys	Asp	Tyr	Ala	Pro	Asn	Asp	Asp	Ser	Val	Arg	Val	Arg	Pro
485															495
Pro	Gln	Val	Ser	Asp	Val	His	Ile	Ser	Asn	Val	Arg	Val	Ser	Asn	Val
500															510
Lys	Thr	Ala	Glu	Gly	Ser	Phe	Ser	Cys	Tyr	Gln	Ala	Met	Val	Leu	Leu
515															525
Gly	Pro	Val	Ala	Ala	Ser	Phe	Asn	Gly	Ala	Pro	Gly	Thr	Ala	Ile	Leu
530															540
Pro	Ile	Thr	Asn	Val	Thr	Val	Ser	Asp	Ser	Asp	Phe	Gly	Thr	Pro	Arg
545															560
Asn	Ser	Ala	Glu	Pro	Trp	Phe	Ala	Phe	Asn	Val	Gln	Gly	Leu	Lys	Leu
565															575
Arg	Asn	Val	Arg	Ile	Asp	Gly	Lys	Glu	Tyr	Asn	Val				
580															585

<210> 77

<211> 2043

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 77

ataaaaacct	ccagagcaat	ttttactaca	tcaacacttt	tacaccgcgc	gcttatacgcg		60
gctagtgtca	gcatggcaat	gagttctgcc	gcatgggcgg	gttgtaccta	tacggtcacc		120
aataattggg	gctcaggatt	taccggcga	atcaaagtga	ccaacaacac	cacccgcagc		180
gtgaacaatt	ggtctgtgtc	atggcaggaa	tccggtgccg	ctatcaccaa	cgccctggaa		240
gcaacgctca	gtggctcaaa	cccttacaca	gccgtatccg	ctgggtggaa	tggcacactt		300
gcccccaatg	catcgccac	tttggtttc	caggcaaacg	gttctgcccgg	tgcaccta		360
gtgaatggca	gcttgcgcgg	caccaacact	tcatcaacac	cggcatccag	cagtgtgcc		420
agctcggtt	aatcaagcgc	gcccgtatcg	tccagcagca	gatcatccag	ttcaatcgct		480
atcactagca	gctcttagc	gagaagttct	attgcctcca	gcagctact	agtttagtagc		540
tccagagcga	gcagtagtgc	gccaagcgtt	ttctctttt	cgatccagga	agagaagcg		600
ggctctgtc	gtgttgcgtt	cattgcaca	gaaagcacca	acaccggttt	tacggcaat		660
ggctacacca	atgcgaacaa	cgcgcaaggc	gcagcgattt	aatgggcagt	cagcgcaccc		720
agcagtggcc	gttatacagt	agcctccgc	ttcgccaatg	gccccacagc	agcgcgcac		780
ggctcggtt	taatcaatgg	cggtagcaat	ggttaattaca	ctgtggagtt	acccctgacc		840
ggcgcatgg	caacctggca	aattgccagc	gtggaaattt	atttagtgca	aggcaataat		900
atttaaaac	tctcgccgtt	aaccgctgac	gtttggcca	atatcgactc	attaaaaata		960
gacggcgcgc	aaaccaaaggc	aggtacttgc	agcactacat	caagcagcag	cggtgcgcagc		1020
agctcgctgt	ccgttaaattc	cagcgcaagt	tcttcttcga	gttcatccac	cgctgcacaa		1080
atactgacat	tagacggtaa	cccgccgcgc	agctggttca	acaaatccag	gaccaagtgg		1140
aatagcagcc	gcccgcgat	tgtgttgtt	taccagcaat	ccaacggcgg	ttggccaaaa		1200
aacctggatt	acaactcagt	gagcgcaggc	aatggcgaaa	gccccacgg	caccatcgac		1260
aatggtgcaa	ccattaccga	aatggtttac	ctcgctgaaa	tttataaaaa	cgccggcaac		1320
accaaataatc	gcgcgcgat	gcccgcgat	gcaaaatttt	tagtgagctc	gcaatacagc		1380
acaggcgcct	tgccacaatt	ttatccgtt	aaaggcggct	atgcggatca	tgcgcaccc		1440
aacgataacg	gcatggcgta	cgcgttgac	gtattggatt	tcgcgttca	caaacgcgc		1500
ccggttgcata	acgcacattt	ctctgattt	gatcgggcga	aattcaaaac	cgctgttgcc		1560
aaaggtgtgg	attacatttt	aaaagcgcag	tggaaacaaa	atggaaaact	cactgcattt		1620
tgtgcacaac	acggtgctac	ggattaccaa	ccgaaaaaaag	cgcgcgccta	tgaattggaa		1680
tcattgagtg	gtagcgagtc	ggtcggcatt	ctcgcccttct	tgtatgacc	accacaaacc		1740
gcccgcgcgt	aagcggcgg	caaggcgggt	gtcaactgg	tcgcgcgtcc	aaataactt		1800
ttggctact	acacttacga	ttcatcaaaa	gcgtctacca	acccgattt	gtataatcc		1860
ggaagcagaa	tgtggatcg	cttctatgac	ctgaacacca	accgtggttt	ctttagtgat		1920
cgcgcgcgt	gcaaaattcta	tgtatcacc	caaatgtcag	aagagcgtcg	cacccgttat		1980
agctgggtt	gctcttacgg	tgaatctatt	atcccttcg	cgcaaaaagt	gggttatctg		2040
taa							2043

<210> 78
 <211> 680
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(33)

<221> BINDING
 <222> (34)...(126)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (199)...(322)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (323)...(680)
 <223> Catalytic domain

<400> 78
 Met Lys Thr Ser Arg Ala Ile Phe Thr Thr Ser Thr Leu Leu His Arg
 1 5 10 15
 Ala Leu Ile Ala Ala Ser Val Ser Met Ala Met Ser Ser Ala Ala Trp
 20 25 30
 Ala Gly Cys Thr Tyr Thr Val Thr Asn Asn Trp Gly Ser Gly Phe Thr
 35 40 45
 Gly Glu Ile Lys Val Thr Asn Asn Thr Thr Ala Ser Val Asn Asn Trp
 50 55 60
 Ser Val Ser Trp Gln Glu Ser Gly Ala Ala Ile Thr Asn Ala Trp Asn
 65 70 75 80
 Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Val Ser Ala Gly Trp
 85 90 95
 Asn Gly Thr Leu Ala Pro Asn Ala Ser Ala Thr Phe Gly Phe Gln Ala
 100 105 110
 Asn Gly Ser Ala Gly Ala Pro Lys Val Asn Gly Ser Leu Cys Gly Thr
 115 120 125
 Asn Thr Ser Ser Thr Pro Ala Ser Ser Ser Val Ala Ser Ser Val Lys
 130 135 140
 Ser Ser Ala Pro Val Ser Ser Ser Arg Ser Ser Ser Ser Ile Ala
 145 150 155 160
 Ile Thr Ser Ser Ser Leu Ala Arg Ser Ser Ile Ala Ser Ser Ser Ser
 165 170 175
 Leu Val Ser Ser Arg Ala Ser Ser Ala Pro Ser Val Phe Ser
 180 185 190
 Phe Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile
 195 200 205
 Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr Asn
 210 215 220
 Ala Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Ser Ala Pro
 225 230 235 240
 Ser Ser Gly Arg Tyr Thr Val Ala Phe Arg Phe Ala Asn Gly Gly Thr
 245 250 255
 Ala Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly Asn
 260 265 270

Tyr Thr Val Glu Leu Pro Leu Thr Gly Ala Trp Ala Thr Trp Gln Ile
 275 280 285
 Ala Ser Val Glu Ile Asp Leu Val Gln Gly Asn Asn Ile Leu Lys Leu
 290 295 300
 Ser Ala Leu Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile
 305 310 315 320
 Asp Gly Ala Gln Thr Lys Ala Gly Thr Cys Ser Thr Thr Ser Ser
 325 330 335
 Ser Val Ala Ser Ser Ser Ser Val Lys Ser Ser Ala Ser Ser Ser
 340 345 350
 Ser Ser Ser Thr Ala Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro
 355 360 365
 Ala Ala Ser Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg
 370 375 380
 Ala Asp Ile Val Leu Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys
 385 390 395 400
 Asn Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser
 405 410 415
 Gly Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala
 420 425 430
 Glu Ile Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg
 435 440 445
 Arg Ala Ala Asn Phe Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu
 450 455 460
 Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe
 465 470 475 480
 Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val
 485 490 495
 Asn Lys Arg Ala Pro Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg
 500 505 510
 Ala Lys Phe Lys Thr Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys
 515 520 525
 Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His
 530 535 540
 Gly Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu
 545 550 555 560
 Ser Leu Ser Gly Ser Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr
 565 570 575
 Gln Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn
 580 585 590
 Trp Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser
 595 600 605
 Ser Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met
 610 615 620
 Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp
 625 630 635 640
 Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg
 645 650 655
 Arg Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser
 660 665 670
 Phe Ala Gln Lys Val Gly Tyr Leu
 675 680

<210> 79
 <211> 1746
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 79

atgacgacac	gacgcgaatt	catcaaaggc	tttctactta	ccggagcagc	cgtggccgtc	60
gctccgcgtt	taattgcgtt	cggcgccggag	gcaagtccgt	ggaaaacgt	gatgccttcg	120
atccctcgac	gcatcacacc	acctcggtt	ccgaaacgca	ccttctatct	caatcgattc	180
ggcgccaaagg	gcgatggagt	cacagactgc	accgcggctt	ttcatcgccg	gatcgatgaa	240
tgcaccaaaag	ccggcggtgg	gaaagtcgtc	gtgcccgg	gcacttatct	caccggcg	300
attcatttga	agagcaacgt	caacctcgaa	gtctcggaaag	gcmcgcacgt	caagttcagt	360
caggaccgaa	aacactac	gcctgttgc	ttctcgcgtt	ggaaagggtt	cgaagtcttc	420
aactactcgc	ctttcattta	cgcgttgcga	cagcgaaaaca	tcgcgatcac	cggcaaaggc	480
acgctcgacg	gacagagtga	ttcggaaacac	tggtgccgt	gaaacggccg	tccgcagttac	540
ggatggaatg	aagggtatgaa	acagcgcgt	cccgatcgca	acgcgttgc	cacaatggcg	600
gagaaaggcg	tgccgggtcg	cgagcgcattc	tttggcgaag	gtcatttattt	gaggccgcag	660
ttcattcgcg	cgtaccgcgt	ccagaacgtg	ctgatccagg	gcgtgacgt	tcggaactcg	720
ccgatgtggg	agatttaccc	ggtgttgc	cgcaacgtg	ctattcacga	cgtgcacatc	780
gatagtcatg	gaccaaaca	cgacggctgc	aatccgaat	cgtgcagcg	cgtgttattt	840
aaggatagct	acttcgat	cggcgacgc	tgcatcgca	tcaaatcggg	acgcaacgccc	900
gacgggcggc	ggcttaaagc	gccgactgag	aacatcatcg	ttaaggatg	tcgcatgaaa	960
gacggccacg	gtggaatcac	ggtcggcagc	gagatctcg	gccccgtgcg	aaacctgttt	1020
gcccagaatt	gccggctcg	cagtccaaac	ctcgatcacg	ccctgcgcgt	gaagaacaat	1080
gccccatgcgcg	gcccattact	cgagaacttc	cacttccgt	acatcgaaat	cgggcagggt	1140
gccccatgcgcg	tgattacat	cgaactcaac	tacgaagagg	gcccggaaagg	gtcgttcacg	1200
ccggcgttgc	gcccattacac	ggtcgtatcg	ttgcgcagca	cgaagagcaa	gcacgcactc	1260
gacgtccagg	gtctgcccgg	cgcgcggcgt	atcaacctgc	gattgacaaa	ctgcacattc	1320
aacgatgtgc	agcaaccgaa	cattctcaag	aacgtcgac	aatcaacctt	tgagaacgtc	1380
acgatatacg	gaaagacgt	cacacaaaca	ggatccatct	cagaaagagc	ggccacgaca	1440
gcaatgaccg	cgcttggcg	cgacgcgtcg	aggaagaaa	acggttatcc	cgcgaagtgg	1500
acctatgatc	atgggctgg	cctgaaagga	atcgagcgcg	tttggaaacaa	tacggcgat	1560
aagaagtatc	tgaagttcat	ccaggacacg	atggaccact	tcgtcaacga	cgacggctcc	1620
attcgacact	acacgatcg	cgagtacaa	atcgatcacg	ttcttccgg	acgaaacctc	1680
ctgttcctt	acaaaactac	cgtcaggaa	aagtatcg	aagccgcgc	gttctgcgc	1740
gaacaa						1746

<210> 80

<211> 582

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(28)

<221> DOMAIN

<222> (81)...(458)

<223> Catalytic domain

<400> 80

Met	Thr	Thr	Arg	Arg	Glu	Phe	Ile	Lys	Gly	Phe	Leu	Leu	Thr	Gly	Ala
1					5			10					15		
Ala	Val	Ala	Val	Ala	Pro	Arg	Leu	Ile	Ala	Phe	Gly	Ala	Glu	Ala	Ser
								20		25			30		
Pro	Trp	Glu	Thr	Met	Met	Pro	Ser	Ile	Leu	Ala	Arg	Ile	Thr	Pro	Pro
								35		40			45		
Arg	Phe	Pro	Lys	Arg	Thr	Phe	Tyr	Leu	Asn	Arg	Phe	Gly	Ala	Lys	Gly
								50		55			60		
Asp	Gly	Val	Thr	Asp	Cys	Thr	Ala	Ala	Phe	His	Arg	Ala	Ile	Asp	Glu

65	70	75	80
Cys Thr Lys Ala Gly Gly Gly Lys Val Val Val Pro Ala Gly Thr Tyr			
85	90	95	
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu Glu Val Ser			
100	105	110	
Glu Gly Ala Thr Ile Lys Phe Ser Gln Asp Pro Lys His Tyr Leu Pro			
115	120	125	
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro			
130	135	140	
Phe Ile Tyr Ala Phe Glu Gln Arg Asn Ile Ala Ile Thr Gly Lys Gly			
145	150	155	160
Thr Leu Asp Gly Gln Ser Asp Ser Glu His Trp Trp Pro Trp Asn Gly			
165	170	175	
Arg Pro Gln Tyr Gly Trp Asn Glu Gly Met Lys Gln Gln Arg Pro Asp			
180	185	190	
Arg Asn Ala Leu Phe Thr Met Ala Glu Lys Gly Val Pro Val Arg Glu			
195	200	205	
Arg Ile Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro			
210	215	220	
Tyr Arg Cys Gln Asn Val Leu Ile Gln Gly Val Thr Ile Arg Asn Ser			
225	230	235	240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Thr Ile His			
245	250	255	
Asp Val His Ile Asp Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro			
260	265	270	
Glu Ser Cys Ser Asp Val Leu Ile Lys Asp Ser Tyr Phe Asp Thr Gly			
275	280	285	
Asp Asp Cys Ile Ala Ile Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg			
290	295	300	
Leu Lys Ala Pro Thr Glu Asn Ile Ile Val Gln Gly Cys Arg Met Lys			
305	310	315	320
Asp Gly His Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val			
325	330	335	
Arg Asn Leu Phe Ala Glu Asn Cys Arg Leu Asp Ser Pro Asn Leu Asp			
340	345	350	
His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly Gly Leu Leu Glu			
355	360	365	
Asn Phe His Phe Arg Asn Ile Glu Val Gly Gln Val Ala His Ala Val			
370	375	380	
Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Phe Thr			
385	390	395	400
Pro Val Val Arg Asp Tyr Thr Val Asp Arg Leu Arg Ser Thr Lys Ser			
405	410	415	
Lys His Ala Leu Asp Val Gln Gly Leu Pro Gly Ala Pro Val Ile Asn			
420	425	430	
Leu Arg Leu Thr Asn Cys Thr Phe Asn Asp Val Gln Gln Pro Asn Ile			
435	440	445	
Leu Lys Asn Val Glu Gln Ser Thr Phe Glu Asn Val Thr Ile Asn Gly			
450	455	460	
Lys Thr Ile Thr Gln Thr Gly Ser Ile Ser Glu Arg Ala Ala Thr Thr			
465	470	475	480
Ala Met Thr Ala Leu Trp Arg Asp Ala Ser Arg Lys Glu Asn Gly Tyr			
485	490	495	
Pro Ala Lys Trp Thr Tyr Asp His Gly Leu Val Leu Lys Gly Ile Glu			
500	505	510	
Arg Val Trp Asn Asn Thr Gly Asp Lys Lys Tyr Leu Lys Phe Ile Gln			
515	520	525	
Asp Ser Met Asp His Phe Val Asn Asp Asp Gly Ser Ile Arg Thr Tyr			
530	535	540	

Thr	Ile	Asp	Glu	Tyr	Asn	Ile	Asp	His	Val	Leu	Pro	Gly	Arg	Asn	Leu
545										555					560
Leu	Phe	Leu	Tyr	Lys	Thr	Thr	Gly	Gln	Glu	Lys	Tyr	Arg	Lys	Ala	Ala
										565					575
Ala	Phe	Leu	Arg	Glu	Gln										
						580									

<210> 81

<211> 1065

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 81

atgacgctac	ccgttgttcc	cctgcgcgtg	ctgctggcgc	tgctggccac	gttggccgtc	60
gcctgcgcg	gcgcgtgcgt	atccgcggca	gcgaccgacc	cggtcgccga	gaacatgctg	120
ctgctgcaga	ccgcctccgg	ttggctggtcc	aagcaactacc	gcgggaagaa	ggtcgactac	180
acgcgcatt	acgcacaccgc	cgagcgcgccc	gcgcgtgcgcg	cgccccggccg	gcatgacgac	240
gcgcacgtcg	acaacaaggc	cacgaccaggc	gagatcgccct	acctggtgca	ggcacatgcc	300
aggacgggca	acccggcgta	cctcgacggt	gccccggcg	gggtcgaata	cctgctgcgc	360
ggcgcagtacc	cgaatgggtg	ctggccgcag	ttctaccccg	accactcgcc	ctaccggcac	420
cagatcacgc	tcaacgcga	cgcgatgggt	catgccccatca	ccgtgctgca	ggacatcgcc	480
gccggccgcg	acggcatgca	ggcgttgacg	cccgagttcg	gcgtccgcgc	cgccgcgcgc	540
ggcgcagcg	gcatcgaaaa	cctgctcgag	ttgcaggtgc	gatcgacgg	cgagccgacc	600
atctggccgc	cgcagtagca	cgagcatagc	ctgcagccgg	ccaaggcccc	cgccatatgaa	660
ctgcccctcg	tggccgtggc	cgaatcggtc	ggcgtggtgc	gcctgctgat	gcccagccg	720
aggccggatg	cccgaggaccgt	cgccgcgatc	gaatcgccgg	cccgctggct	ggaggcgcat	780
ccgcctgcatg	acctggcgct	cgaacgcgtc	gacgcaccgg	ccgaggaaac	ggcaaggac	840
gtgcgggtcg	tgacccggcc	cggcgccctcg	ctgtggcgcc	gcttctacga	cctggatgga	900
cagcagccctc	tgttcgtcga	ccgcgacagc	aagccgtcc	cgttcgccag	cctgccccaa	960
gagcggccgca	ccggctatgc	ctggtacggc	acctggccgg	agaagctgct	ggcgaggaa	1020
ctcccgcgct	ggcgcgaggt	ccatgcccc	ggcgccgcgc	cctgaa		1065

<210> 82

<211> 354

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(30)

<221> DOMAIN

<222> (31)...(354)

<223> Catalytic domain

<400> 82

Met	Thr	Leu	Pro	Val	Val	Ser	Leu	Arg	Val	Leu	Leu	Ala	Leu	Leu	Ala
1				5					10			15			
Thr	Leu	Pro	Val	Ala	Cys	Ala	Gly	Ala	Ala	Val	Ser	Ala	Ala	Ala	Thr
									20		25		30		
Asp	Pro	Val	Ala	Glu	Asn	Met	Leu	Leu	Leu	Gln	Thr	Ala	Ser	Gly	Gly
									35		40		45		
Trp	Ser	Lys	His	Tyr	Arg	Gly	Lys	Lys	Val	Asp	Tyr	Thr	Arg	Asn	Tyr
									50		55		60		

Asp Thr Ala Glu Arg Ala Ala Leu Arg Ala Pro Gly Arg His Asp Asp
 65 70 75 80
 Ala Thr Ile Asp Asn Lys Ala Thr Thr Ser Glu Ile Ala Tyr Leu Val
 85 90 95
 Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
 100 105 110
 Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
 115 120 125
 Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
 130 135 140
 Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
 145 150 155 160
 Ala Gly Arg Asp Gly Met Gln Ala Leu Thr Pro Glu Phe Gly Val Arg
 165 170 175
 Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
 180 185 190
 Val Arg Ile Asp Gly Glu Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
 195 200 205
 His Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
 210 215 220
 Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
 225 230 235 240
 Arg Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ser Ala Ala Arg Trp
 245 250 255
 Leu Glu Ala His Arg Leu His Asp Leu Ala Leu Glu Arg Val Asp Ala
 260 265 270
 Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Thr Arg Pro Gly
 275 280 285
 Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Asp Gly Gln Gln Pro Leu
 290 295 300
 Phe Val Asp Arg Asp Ser Lys Pro Val Pro Phe Ala Ser Leu Pro Asn
 305 310 315 320
 Glu Arg Arg Thr Gly Tyr Ala Trp Tyr Gly Thr Trp Pro Glu Lys Leu
 325 330 335
 Leu Ala Gln Glu Leu Pro Arg Trp Arg Glu Val His Ala Ala Gly Ala
 340 345 350
 Ala Pro

<210> 83

<211> 3618

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 83

ttgactgct	tttcaagaaa	cagtcagggt	gatgttaagct	gggaaccgag	ttccgccccaa	60
caggtaacct	acaatctaaa	acgcagtacc	acgaaggagg	gtccttatca	gaccattgct	120
gaaaaaatgg	cagaaaccga	cttccggat	acagggttag	agaatggcca	gaagtattac	180
tatgttgtat	ctgccaaac	gagtagcggt	gagagtgcag	attcacaagc	tataacggct	240
gtgcctgtag	cgcatttgc	agctccgacc	ggccttcag	caagtcatgg	caatggcgaa	300
gttaaccattc	attggaaatc	cgtcaatggt	gccgagtctt	accaagtctt	gcgcagtaaa	360
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accgggattc	ccgatggcga	gaagtactat	tatgtcgtat	ccgccaagaa	cgatacagct	480
gaaagtgc当地	attcccaacc	gattaacggt	gctgctgtat	cgacgagtgg	tgtaccagcc	540
attccaaacg	gtatgaacgc	tactgccgg	gatggcagag	ctgccttaac	ctggcccgct	600
gtatccggcg	cagattccta	tagcatcaag	cgcggtgagt	ttaacagtgg	tcaatatgag	660

gtcattgcta	aaaatataca	ctctaccggt	tatcaagata	taggccttac	aaacggtgat	720
acctatgatt	atgtgatttc	cgctgtcaat	gagcaagggg	aaagtttagg	ctccgaaccc	780
atcgccgtta	ctcctgcgaa	agtaacgggt	gtagcggaaag	aaggcggaga	ctttaaaacg	840
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cagattgatg	atgcattggg	ccgtgggctg	gattatgt	taaaatcgc	aattaaggta	3060
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cgcggattt	tctcaggaag	agacgggtgc	attaaacaca	acatctttaga	gattaaaaaa	3420
gaaagaagag	acggctaccg	ctgggcagga	gaatgccgc	aaaaattatt	aaatatcgcc	3480
aacacaactg	gctactacga	aaacagagta	tacgtagaag	tcgttggg	tcagtctaaa	3540
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ggttctacaa	gcaagtaa					3618

<210> 84

<211> 1205

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN
 <222> (268)...(556)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (782)...(1164)
 <223> Catalytic domain

<400> 84
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 1 5 10 15
 Ser Ser Ala Gln Gln Val Thr Tyr Asn Leu Lys Arg Ser Thr Thr Lys
 20 25 30
 Glu Gly Pro Tyr Gln Thr Ile Ala Glu Lys Met Ala Glu Thr Asp Phe
 35 40 45
 Arg Asp Thr Gly Leu Glu Asn Gly Gln Lys Tyr Tyr Val Val Ser
 50 55 60
 Ala Glu Thr Ser Ser Gly Glu Ser Ala Asp Ser Gln Ala Ile Thr Ala
 65 70 75 80
 Val Pro Val Ala Pro Leu Gln Ala Pro Thr Gly Leu Ser Ala Ser His
 85 90 95
 Gly Asn Gly Gly Val Thr Ile His Trp Glu Ser Val Asn Gly Ala Glu
 100 105 110
 Ser Tyr Gln Val Leu Arg Ser Lys Gln Lys Gly Ile Gly Tyr Glu Val
 115 120 125
 Ile Lys Asn Gly Val Thr Glu Thr Ser Tyr Thr Asp Thr Gly Ile Pro
 130 135 140
 Asp Gly Glu Lys Tyr Tyr Val Val Ser Ala Lys Asn Asp Thr Ala
 145 150 155 160
 Glu Ser Ala Asn Ser Gln Pro Ile Asn Gly Ala Ala Val Ser Thr Ser
 165 170 175
 Gly Val Pro Ala Ile Pro Asn Gly Met Asn Ala Thr Ala Gly Asp Gly
 180 185 190
 Arg Ala Ala Leu Thr Trp Ser Ala Val Ser Gly Ala Asp Ser Tyr Ser
 195 200 205
 Ile Lys Arg Gly Glu Phe Asn Ser Gly Gln Tyr Glu Val Ile Ala Lys
 210 215 220
 Asn Ile His Ser Thr Gly Tyr Gln Asp Ile Gly Leu Thr Asn Gly Asp
 225 230 235 240
 Thr Tyr Asp Tyr Val Ile Ser Ala Val Asn Glu Gln Gly Glu Ser Leu
 245 250 255
 Gly Ser Glu Pro Ile Ala Val Thr Pro Ala Lys Val Thr Val Val Ala
 260 265 270
 Lys Glu Gly Gly Asp Phe Lys Thr Ile Gln Glu Ala Ile Asp Ala Ala
 275 280 285
 Pro Asp Asn Ser Thr Lys Arg His Val Ile Phe Ile Lys Asn Gly Gln
 290 295 300
 Tyr Arg Glu Lys Leu Thr Ile Pro Lys Ser Lys Thr Asn Leu Ser Phe
 305 310 315 320
 Val Gly Glu Ser Lys Glu Gly Thr Val Leu Val Phe Asn Asp Asn Ala
 325 330 335
 Asn Thr Pro Gly Pro Asp Gly Lys Pro Leu Gly Thr Ser Asn Ser Ser
 340 345 350
 Ser Ile Phe Ile Tyr Ala Asn Asp Phe Ile Ala Gln Asn Leu Thr Ile
 355 360 365
 Gln Asn Asp Ser Gly Gln Gly Thr Gly Gln Ala Val Ala Ala Tyr Val
 370 375 380
 Arg Ala Asp Arg Leu Tyr Phe Glu Asn Val Gln Phe Leu Gly Tyr Gln
 385 390 395 400

Asp Thr Leu Tyr Ala His Thr Gly Arg Gln Tyr Tyr Lys Asn Cys Tyr
 405 410 415
 Val Glu Gly Asp Val Asp Phe Ile Phe Gly Gly Ala Thr Ala Leu Phe
 420 425 430
 Asp Thr Cys His Leu His Ser Lys Arg Thr Gly Ser Lys Leu Thr Ala
 435 440 445
 Ala Ser Thr Asp Gln Val Thr Pro Tyr Gly Tyr Val Phe Leu Asp Ser
 450 455 460
 Lys Ile Thr Ser Asp Glu Gly Val Thr Asn Val His Leu Gly Arg Pro
 465 470 475 480
 Trp Arg Pro Tyr Ser Ala Val Thr Tyr Ile Asn Thr Glu Met Asp Ala
 485 490 495
 Ser Ile Val Pro Asp Gly Trp Asp Asn Trp Gly Lys Val Glu Asn Glu
 500 505 510
 Lys Thr Ala Arg Tyr Ser Glu Tyr Asn Asn Met Gly Pro Gly Ala Asp
 515 520 525
 Pro Lys Lys Arg Asp Pro Trp Thr Thr Gln Leu Thr Pro Glu Glu Ala
 530 535 540
 Asn Gln Tyr Thr Val Gln Asn Val Met Lys Gly Ser Asp Gly Trp Asp
 545 550 555 560
 Pro Glu Arg Ile Gly Ile Ile Pro Leu Ser Pro Leu Ser Ala Pro Ile
 565 570 575
 Ile Ser Leu Asp Gln Arg Asp Ser Ile Val Asn Thr Pro Ser Phe Thr
 580 585 590
 Ile Thr Gly Gln Val Asp Lys Glu Ala Ala Val Ser Val Asn Gly Lys
 595 600 605
 Glu Ile Ser Leu Gln Lys Asp Gly Ser Phe Ser Thr Thr Val Val Leu
 610 615 620
 Asn Asp Gly Leu Asn Thr Ile Thr Val Gly Ala Val Asp Ala Ala Gly
 625 630 635 640
 Asn Gln Ala Ile Pro Ala Val Leu Lys Ile Val Tyr Asp His Glu Lys
 645 650 655
 Pro Val Val Ser Ile Asp Asp Leu Lys Gly Glu Lys Asn Gly Asn His
 660 665 670
 Tyr Asn Val Ile Tyr Asn Pro Leu Pro Ile Thr Gly Lys Leu Asn Glu
 675 680 685
 Ala Gly Thr Val Met Val Asn Gly Glu Lys Val Asn Val Ser Glu Lys
 690 695 700
 Leu Thr Phe Ser Thr Lys Val Ile Leu Lys Pro Gly Leu Asn Asn Ile
 705 710 715 720
 Thr Ile Thr Ala Val Asp Gln Ala Gly Asn Glu Ala Glu Ser Ile Thr
 725 730 735
 Ile Asn Val Val Pro Lys Gly Asn Ala Val Pro Asp Gly Pro Val Lys
 740 745 750
 Ile Ile Lys Ser Glu Thr Thr Asn Ala Asn Thr Val Glu Val Thr Phe
 755 760 765
 Asn Ser Lys Leu Glu Lys Phe Asp Ser Ser Asp Ile Ala Leu Gln Thr
 770 775 780
 Ala Thr Asn Val Trp Ala Ala Leu Asn Pro Gly Leu Lys Gln Leu Met
 785 790 795 800
 Thr Val Glu Ser Ile Thr Thr Lys Val Asn Lys Asp Asn Gln Thr Val
 805 810 815
 Ala Val Ile Lys Thr Lys Glu Ala Phe Gln Glu Asp Gly Thr Ile Thr
 820 825 830
 Leu Pro Lys Val Glu Asp Pro Phe His Ile Gln Tyr Leu Asn Ala Asp
 835 840 845
 Tyr Tyr Thr Gly Asp Arg Thr Gln Asp Ile Lys His Ala Asp Ala Leu
 850 855 860
 Leu Thr Trp Gln Met Asp His Gly Gly Trp Phe Lys Asn Trp Val Glu

865	870	875	880
Lys	Tyr	Lys	Arg
885	890	895	
Ser	Thr	Asn	His
900	905	910	
Asn	Glu	Ile	Leu
915	920	925	
Arg	Tyr	Lys	Asp
930	935	940	
Gln	Val	Asp	Ser
945	950	955	960
Tyr	Ser	Asp	Tyr
965	970	975	
Ser	Val	Leu	Thr
980	985	990	
Leu	Gly	Asp	Glu
995	1000	1005	
Gly	Leu	Asp	Tyr
1010	1015	1020	
Thr	Ala	Trp	Cys
1025	1030	1035	1040
Ala	Arg	Ala	Tyr
1045	1050	1055	
Ile	Val	Gln	Tyr
1060	1065	1070	
Ala	Ala	Ile	His
1075	1080	1085	
Gly	Thr	Lys	Tyr
1090	1095	1100	
Asp	Ala	Asn	Ser
1105	1110	1115	1120
Arg	Pro	Ile	Phe
1125	1130	1135	
Glu	Ile	Glu	Lys
1140	1145	1150	
Pro	Gln	Lys	Leu
1155	1160	1165	
Arg	Val	Tyr	Val
1170	1175	1180	
Glu	Ser	Leu	Glu
1185	1190	1195	1200
Gly	Ser	Thr	Ser
1205			

<210> 85

<211> 1152

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 85

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tctaaagaaaa	atgatcagga	agtccggcgcg	atcgcgtgga	aagatgcaca	tggaaagccg	180
gatgagtgggt	atgcgagtgt	tgagggactg	cggatggccg	ataacgtcgt	tctcttatcaa	240
cgcgactcag	gtgggtggcc	caagaacatc	gacatggcga	aggcactcaa	cgatcgtgag	300
caggctgcga	tcctccgcca	gaagaaaaag	aacgactcca	cgatcgacaa	tggtgcgact	360

cacacacagt tataccttctt	ggcgccgcgtc	tatacagcac	agcgtcagga	gcgacatcgc	420
gagtcgtttt	tcaaaggatt	ggattactta	ctgaatgcgc	agtatccaaa	480
cccgagttt	atccgaaccc	gacgggctat	cacaagcaca	ttacttacaa	540
atgattggtg	tgatgaaggt	gctgcgcgtat	atcgctgcgg	cgaaggcttt	600
gtcgcacgaag	ctcggcgcgc	gaaggcgcacg	agtgcagttg	aaaaaggat	660
ttgaaaacgc	aggtgggtt	agatgggcgt	cgcactgtgt	ggagtgcgca	720
gtaacgttag	cggcagctcc	tgcgcgaacc	ttcgagttaa	cttcgttgag	780
agcgttagata	tcgttcgatt	ttaatgtcg	atcaaggatc	cgtcgcctaa	840
gcgggttaat	cggcggtttaa	gtgggttgag	caatcgagtt	taaaaggctg	900
aagaaggcgg	acgcttctaa	acctggcggg	tttgattgcg	tcgttagttaa	960
agctcggtt	gggcgcgtt	ttatgagatt	ggcacacaacc	ggccgatctt	1020
gatggagtgg	tcaaatacga	cgtggcgcag	atcgAACACG	agcggcggac	1080
tggtagttt	atgaagcagc	caagctgctg	aagaaagagt	atccggcctg	1140
acatctctgt	ga				1152

<210> 86

<211> 383

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(383)

<223> Catalytic domain

<400> 86

Met	Ser	Val	Gly	Pro	Gly	Ala	Asn	Pro	Lys	Ala	Arg	Val	Pro	Trp	Ser
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Lys	Gln	Leu	Ser	Gly	Val	Ala	Lys	Leu	Phe	Gln	Arg	Glu	Arg	Phe	
			20				25				30				
Phe	Ser	Leu	Ala	Ala	Glu	His	Thr	Ser	Lys	Lys	Asn	Asp	Gln	Glu	Val
			35				40				45				
Gly	Ala	Ile	Ala	Trp	Lys	Asp	Ala	His	Gly	Lys	Pro	Asp	Glu	Trp	Tyr
			50			55				60					
Ala	Ser	Val	Glu	Ala	Leu	Arg	Met	Ala	Asp	Asn	Val	Val	Leu	Tyr	Gln
			65			70			75					80	
Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Ala	Lys	Ala	Leu
				85				90					95		
Asn	Asp	Arg	Glu	Gln	Ala	Ala	Ile	Leu	Arg	Gln	Lys	Lys	Lys	Asn	Asp
				100				105					110		
Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	His	Thr	Gln	Leu	Ser	Phe	Leu	Ala
					115			120				125			
Arg	Val	Tyr	Thr	Ala	Gln	Arg	Gln	Glu	Arg	His	Arg	Glu	Ser	Phe	Phe
				130			135			140					
Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Asn	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp
				145			150			155				160	
Pro	Gln	Phe	Tyr	Pro	Asn	Pro	Thr	Gly	Tyr	His	Lys	His	Ile	Thr	Tyr
				165				170					175		
Asn	Asp	Gly	Ala	Met	Ile	Gly	Val	Met	Lys	Val	Leu	Arg	Asp	Ile	Ala
				180			185				190				
Ala	Ala	Lys	Pro	Leu	Tyr	Ala	Phe	Val	Asp	Glu	Ala	Arg	Arg	Ala	Lys
				195			200			205					
Ala	Thr	Ser	Ala	Val	Glu	Lys	Gly	Ile	Glu	Cys	Ile	Leu	Lys	Thr	Gln
				210			215			220					
Val	Val	Val	Asp	Gly	Arg	Arg	Thr	Val	Trp	Ser	Ala	Gln	His	Asp	Glu
			225			230			235					240	
Val	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Thr	Phe	Glu	Leu	Thr	Ser	Leu

	245	250	255
Ser Gly Gly Glu Ser Val Asp Ile Val Arg Phe Leu Met Ser Ile Lys			
260	265	270	
Asp Pro Ser Pro Lys Val Val Asp Ala Val Glu Ser Ala Val Lys Trp			
275	280	285	
Phe Glu Gln Ser Glu Leu Lys Gly Val Lys Trp Val Lys Lys Ala Asp			
290	295	300	
Ala Ser Lys Pro Gly Gly Phe Asp Cys Val Val Lys Asp Pro Glu			
305	310	315	320
Ser Ser Val Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Ile			
325	330	335	
Phe Ser Gly Arg Asp Gly Val Val Lys Tyr Asp Val Ala Gln Ile Glu			
340	345	350	
His Glu Arg Arg Thr Asn Tyr Glu Trp Tyr Val Asp Glu Ala Ala Lys			
355	360	365	
Leu Leu Lys Lys Glu Tyr Pro Ala Trp Arg Lys Arg Thr Ser Leu			
370	375	380	

<210> 87

<211> 1698

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 87

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gcagtggcga tggggcagg ttcttcagta ttgcgcggg ctacagggtt tttttccacg	120
actgatggcg gtgcggcaag cggctcgcaa tccttacgg cggccaaact tgaccagctc	180
aacaccattt ttgccaatgc gaagagtggc ggttacccgg ttgtgattac ctataccgg	240
aatgaagaca gcttgattaa ccagatgatc aaagaccaca cctgtggatc ttcaaggcaac	300
tgcccaacc caccgtggag tggaaacctac cgcaaggtag aaattaagga gatgaccaaa	360
ggtgtcacca tcatcggtgc caatggttt tcggccaaact tcgggtattgt ggtgaacaag	420
tccagcaatg tgattatccg caacatgaaa atcggtgcc tcggccgggtc cagcaacgac	480
gccccatata ttcgtatcga tagcggact aacgtatggg ttgaccacaa cgaattgttc	540
gccccatata acaatgtaa aggttcaccg gatggcgatt tgacccctcg aagcgccatc	600
gacatcaaga aagattcaca caacatcacc gtgtcttaca acctgattcg cgacagcaaa	660
aaagtggcc ttgtatggtc cagcggcgc gatatcgcc tcggccggcgtc gatcaacttc	720
caccacaaca tttacaaaaa cgtgaatcga cgcttgcgt tgcaacgcgg tggctggacg	780
cacatgtata acaaccgtta cgacggcatt accgggtccg gatcaacgt acgtcaggcc	840
ggttatgcgt tgattgaaag caactggttt caaaatgcgg ttaacccgtt gacttgcgt	900
tacgacagca gcaactgcgg ttctggat ctgcgcata acaacgtgaa gtcggcagca	960
gatttcgcga cctataacat cacctggacc agcggcggca ctattgtatc aaccaactgg	1020
acgaccaccc ctccgttccc gatcggcatt ctttacagct actcgccgt gtctccacag	1080
tgcgtgaagg acaagttggc cagcgttgc ggtgtggta aaaacgggtc agttctgaac	1140
tcatcgtgt gtgggtggaa cagctctgtt ccatcatcaa gtcagtcgc tactacttcc	1200
aaatcatcca gctcggttagc aaccagcaag tccagctccg tcgctacgac gtccagtaag	1260
tcatccagct cggtagtgcc atcatcatca agctcaagtt cagtggttaa taacggcagc	1320
atcgcgtaa ccggcactgc taccggcaat agcattgtcc tgagctggc gccgaacaac	1380
ctgacactgg gcacccagga ggtgtatcgc gataccgatt cagacccaaag tggccgtgt	1440
cgtattgtcg ccctgagttc cagcactcgc atgtacaccg atgccactgc atcggcgggc	1500
caaacgttct actactggat caaaaacacc accaacggtg taaccaccaa ttccaatgcg	1560
gcttcggcgg caattggcga tgcagctcg gccattcgcc catgcgcagg aaaccgagga	1620
atggcgctc gcaccaggctc cgcagttcg actgggtcaa atcctcggtt gcctgcccgt	1680
accatccca gagcttga	1698

<210> 88

<211> 565

<212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(32)

<221> DOMAIN
 <222> (33)...(375)
 <223> Catalytic domain

<400> 88
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 Ala Val Ala Ala Ala Val Ala Met Phe Ala Gly Ser Ser Val Phe Ala
 20 25 30
 Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Ala Ala Ser Gly
 35 40 45
 Ser Gln Ser Phe Thr Ala Ala Asn Leu Asp Gln Leu Asn Thr Ile Val
 50 55 60
 Ala Asn Ala Lys Ser Gly Gly Tyr Pro Val Val Ile Thr Tyr Thr Gly
 65 70 75 80
 Asn Glu Asp Ser Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asp
 85 90 95
 Ser Ser Gly Asn Cys Pro Asn Pro Arg Trp Ser Glu Thr Tyr Arg Lys
 100 105 110
 Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Ile Gly Ala Asn
 115 120 125
 Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser Ser Asn Val
 130 135 140
 Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Ala Gly Ala Ser Asn Asp
 145 150 155 160
 Ala Asp Met Ile Arg Ile Asp Ser Gly Thr Asn Val Trp Val Asp His
 165 170 175
 Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser Pro Asp Gly
 180 185 190
 Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Asp Ser His Asn
 195 200 205
 Ile Thr Val Ser Tyr Asn Leu Ile Arg Asp Ser Lys Lys Val Gly Leu
 210 215 220
 Asp Gly Ser Ser Ser Asp Ile Ala Gly Gly Arg Glu Ile Thr Phe
 225 230 235 240
 His His Asn Ile Tyr Lys Asn Val Asn Ala Arg Leu Pro Leu Gln Arg
 245 250 255
 Gly Gly Trp Thr His Met Tyr Asn Asn Leu Tyr Asp Gly Ile Thr Gly
 260 265 270
 Ser Gly Ile Asn Val Arg Gln Ala Gly Tyr Ala Leu Ile Glu Ser Asn
 275 280 285
 Trp Phe Gln Asn Ala Val Asn Pro Val Thr Cys Arg Tyr Asp Ser Ser
 290 295 300
 Asn Cys Gly Phe Trp Asp Leu Arg Asn Asn Asn Val Lys Ser Pro Ala
 305 310 315 320
 Asp Phe Ala Thr Tyr Asn Ile Thr Trp Thr Ser Gly Gly Thr Ile Asp
 325 330 335
 Ala Thr Asn Trp Thr Thr Ala Pro Phe Pro Ile Ser Ile Pro Tyr
 340 345 350
 Ser Tyr Ser Pro Val Ser Pro Gln Cys Val Lys Asp Lys Leu Ala Ser

355	360	365
Val Ala Gly Val Gly Lys Asn Gly Ala Val Leu Asn Ser Ser Val Cys		
370	375	380
Gly Gly Ser Ser Ser Val Pro Ser Ser Ser Val Ala Thr Thr Ser		
385	390	395
Lys Ser Ser Ser Ser Val Ala Thr Ser Lys Ser Ser Ser Val Ala Thr		400
405	410	415
Thr Ser Ser Lys Ser Ser Ser Val Val Pro Ser Ser Ser Ser		
420	425	430
Ser Ser Val Val Asn Asn Gly Ser Ile Ala Leu Thr Ala Thr Ala Thr		
435	440	445
Gly Asn Ser Ile Val Leu Ser Trp Ser Pro Asn Asn Leu Thr Leu Gly		
450	455	460
Thr Gln Glu Val Tyr Arg Asp Thr Asp Ser Asp Pro Ser Gly Arg Val		
465	470	475
Arg Ile Ala Ala Leu Ser Ser Ser Thr Arg Met Tyr Thr Asp Ala Thr		480
485	490	495
Ala Ser Ala Gly Gin Thr Phe Tyr Tyr Trp Ile Lys Asn Thr Thr Asn		
500	505	510
Gly Val Thr Thr Asn Ser Asn Ala Ala Ser Ala Ile Gly Asp Ala		
515	520	525
Ala Arg Ala Ile Arg Ala Cys Ala Gly Asn Arg Gly Ser Gly Ala Arg		
530	535	540
Thr Ser Arg Ala Val Ser Thr Gly Ser Asn Pro Arg Gly Pro Ala Gly		
545	550	560
Ser His Pro Arg Ala		
565		

<210> 89

<211> 1377

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 89

atgacgacgc gacgcaatt cattcgagat cttttggttg gcggcgtagt ggtcgctgtt	60
gcaccgcgtt tcctggcggtt ttcttcgggt gcgagtccgt gggaaacggt gatgccttcg	120
atccctcgaaac gcatcaagcc accgcgtttt ccgaaacgca cgtgctatct caaccgggtt	180
ggagcaaaag ggcacggca aactgattgc acttcagctt ttcgacgcgc aatcgatcag	240
tgttcgaaag cgggcgggtgg caaagtgatc gttccgcagg gaatgtatct caccggcgca	300
attcacttga agagcaacgt caatctcgag atctccgaag gcgcgacgat caagttcagt	360
caaaaacccga aagactatct cccgggtggtt tttcgcgtt gggaggcgt cgaagtattc	420
aactactcac ctttcatcta cgcatggaa cagcagaaca tcgcgatcac gggcaagggc	480
acgctcgatg ggcagagtga taacgaacac tggtgccat ggaacggacg cgccaggtac	540
ggttggaaag aaggatgag ccaccagcgt ccggatcgaa acgcgcttt tgcgatggcg	600
gaaaaagggtg tttcggttcg cgaacgtgtt ttcggcgagg gtcattactt aaggcccgag	660
ttcattcagc cgtatcgctg ccagaacgta ttgatcgacg gagttacgat acgaaactcg	720
ccgatgtggg aaattcatcc ggtgctgtgc cgaaatgtca tcgtgcaaaa cgtgcacatt	780
aacagtcatg gaccaaacaa cgatggctgc aatcccgagt cgtgcactga tgcgtctt	840
aagaactgtt acttcgacac tggcgacgac tgcattcgccg tcaaattcagg acgcaacgcg	900
gacggccggc ggcttaaagc gcccacagag aacgtgatcg tgcaagactg tcaaattgaaa	960
gatggacacg gcgggatcac tgcggcagt gagatctcg gcggtgtgag aaatctgttt	1020
gccccgaaact gcccggcttga tagtccaaac ctggaccatg ctttgcgggt taagaacaac	1080
gcgatgcgtg gaggcgtctcg cggaaatttg cacttccgaa acatcgaaat tggtcagggt	1140
gcccgtggcgg tgcgtacac tgcgtatggt ttgcgcagca cgcgaagcaa atacgcgcctc	1200
ccggcgggttc gtgactacac tgcgtatggt ttgcgcagca cgcgaagcaa atacgcgcctc	1260
gacgttcaag gtctgtcggtt cgcgcgcgatc gtaaatctgc gtctgacgaa ttgcacgttc	1320

gacaatgttgcgaaaggaa cgtcgtaag aatgttaagg acgcgacaat tcaaaaaa 1377

<210> 90
<211> 459
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> DOMAIN
<222> (32)...(459)
<223> Catalytic domain

<400> 90
Met Thr Thr Arg Arg Glu Phe Ile Arg Asp Leu Leu Val Gly Gly Val
1 5 10 15
Val Val Ala Val Ala Pro Arg Phe Leu Ala Phe Ser Ser Val Ala Ser
20 25 30
Pro Trp Glu Thr Val Met Pro Ser Ile Leu Glu Arg Ile Lys Pro Pro
35 40 45
Arg Phe Pro Lys Arg Thr Cys Tyr Leu Asn Arg Phe Gly Ala Lys Gly
50 55 60
Asp Gly Gln Thr Asp Cys Thr Ser Ala Phe Arg Arg Ala Ile Asp Gln
65 70 75 80
Cys Ser Lys Ala Gly Gly Lys Val Ile Val Pro Gln Gly Met Tyr
85 90 95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu Glu Ile Ser
100 105 110
Glu Gly Ala Thr Ile Lys Phe Ser Gln Asn Pro Lys Asp Tyr Leu Pro
115 120 125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
130 135 140
Phe Ile Tyr Ala Phe Glu Gln Gln Asn Ile Ala Ile Thr Gly Lys Gly
145 150 155 160
Thr Leu Asp Gly Gln Ser Asp Asn Glu His Trp Trp Pro Trp Asn Gly
165 170 175
Arg Ala Arg Tyr Gly Trp Lys Glu Gly Met Ser His Gln Arg Pro Asp
180 185 190
Arg Asn Ala Leu Phe Ala Met Ala Glu Lys Gly Val Ser Val Arg Glu
195 200 205
Arg Val Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
210 215 220
Tyr Arg Cys Gln Asn Val Leu Ile Asp Gly Val Thr Ile Arg Asn Ser
225 230 235 240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Ile Val Gln
245 250 255
Asn Val His Ile Asn Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
260 265 270
Glu Ser Cys Thr Asp Val Leu Ile Lys Asn Cys Tyr Phe Asp Thr Gly
275 280 285
Asp Asp Cys Ile Ala Val Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
290 295 300
Leu Lys Ala Pro Thr Glu Asn Val Ile Val Gln Asp Cys Gln Met Lys
305 310 315 320
Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val

325	330	335
Arg Asn Leu Phe Ala Glu Asn Cys Arg	Leu Asp Ser Pro Asn Leu Asp	
340	345	350
His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly	Gly Leu Leu Glu	
355	360	365
Asn Leu His Phe Arg Asn Ile Glu Val Gly Gln	Val Ala His Ala Val	
370	375	380
Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala	Lys Gly Ser Phe Thr	
385	390	400
Pro Val Val Arg Asp Tyr Thr Val Asp Gly	Leu Arg Ser Thr Arg Ser	
405	410	415
Lys Tyr Ala Leu Asp Val Gln Gly	Leu Ser Gly Ala Pro Ile Val Asn	
420	425	430
Leu Arg Leu Thr Asn Cys Thr Phe Asp Asn Val Ala	Glu Gly Asn Val	
435	440	445
Val Lys Asn Val Lys Asp Ala Thr Ile Gln Lys		
450	455	

<210> 91

<211> 1125

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 91	60
gtggtcctag gtaataacgg cggcagcttg agttgcgtcc aatataattgt gattgtgaaa	120
ggacccggtg gacctcgacc gccggtaaa ccggccgtcc aggcggccgt tagggttacc	180
tggagcgcat ccctagcca gcccggcggaa tggtacggga gtgacgaagc gatccgcattc	240
gcggacaaacg tcctcctcta ccagcgcac accggcgggt ggccgaaggg catagatatg	300
gcccggccca tccggaaaca caggaagtcc tttttctca ccgagaaggg gcggaccgat	360
gactcgacca tcgacaacgg tgccaccgtg acccagctca agtatctcgcc cgccgtctac	420
aaggcgacca ggctgaaacg gttcaaggag ggcttctca aaggctctcgat ctacctcttg	480
gcccggccagt acccgaacgg cgctggccc cagtattatc ctaacttggat gggctactac	540
gccaacatca cttataacga caatggcatg gtgaacgtgc tcaccctctt ccagagcatc	600
gccaatgggg ccccgagta cgacttcgtc gacccggcgc gcccggagaa ggccggccgg	660
gcccgtggca aagggtatcgat ctgcatttc aagaccaga tccgtgtcaa tggaaaactt	720
accgccttgtt gcgcccaagc tgacgccaag acgctggcgc ccgcgcggc ccgttctgtat	780
gagctttagt ccatcagcgg tttcgagagc gtcggatcg tccgggttctt aatgagcctc	840
gagaatccga gcccgaaggt catcgaggcg gtagaggccg ccgtgaaatg gttcgaggag	900
gtcaagctta cgggatcaa ggtggtcgag aaacccgacc cgtcccttcc gggcggttac	960
gaccgcgtgg tggtcgaaga ccccaacgcg ccgcggatct gggccgggtt ctacgagatc	1020
ggcaccaccg gtcccttctt ctgcggccgc gatggatca aaaaatacag cctggcggag	1080
atcgaacacg aacgcgggtt cgttactcc tggtacacca atgccccggc ctacctcatc	
gagaaggagt atccgctctg gcgccaaa caccctacca agtaa	1125

<210> 92

<211> 374

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(374)

<400> 92

Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
 1 5 10 15
 Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
 20 25 30
 Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Ser Leu Val Gln Arg
 35 40 45
 Pro Glu Trp Tyr Gly Ser Asp Glu Ala Ile Arg Ile Ala Asp Asn Val
 50 55 60
 Leu Leu Tyr Gln Arg Asn Thr Gly Gly Trp Pro Lys Asp Ile Asp Met
 65 70 75 80
 Ala Glu Pro Ile Pro Glu His Arg Lys Ser Phe Phe Leu Thr Glu Lys
 85 90 95
 Glu Arg Thr Asp Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Gln
 100 105 110
 Leu Lys Tyr Leu Ala Arg Val Tyr Lys Ala Thr Arg Leu Glu Arg Phe
 115 120 125
 Lys Glu Gly Phe Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
 130 135 140
 Pro Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Asn Leu Arg Gly Tyr Tyr
 145 150 155 160
 Ala Asn Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Leu
 165 170 175
 Leu Gln Ser Ile Ala Lys Lys Ala Pro Glu Tyr Asp Phe Val Asp Pro
 180 185 190
 Ala Arg Arg Glu Lys Ala Ala Arg Ala Val Ala Lys Gly Ile Asp Cys
 195 200 205
 Ile Leu Lys Thr Gln Ile Arg Val Asn Gly Lys Leu Thr Ala Trp Cys
 210 215 220
 Ala Gln His Asp Ala Lys Thr Leu Ala Pro Ala Pro Ala Arg Ser Tyr
 225 230 235 240
 Glu Leu Glu Ser Ile Ser Gly Phe Glu Ser Val Gly Ile Val Arg Phe
 245 250 255
 Leu Met Ser Leu Glu Asn Pro Ser Pro Lys Val Ile Glu Ala Val Glu
 260 265 270
 Ala Ala Val Lys Trp Phe Glu Glu Val Lys Leu Thr Gly Ile Lys Val
 275 280 285
 Val Glu Lys Pro Asp Pro Ser Leu Pro Gly Gly Tyr Asp Arg Val Val
 290 295 300
 Val Glu Asp Pro Asn Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile
 305 310 315 320
 Gly Thr Asn Arg Pro Phe Phe Cys Gly Arg Asp Gly Ile Lys Lys Tyr
 325 330 335
 Ser Leu Ala Glu Ile Glu His Glu Arg Arg Val Gly Tyr Ser Trp Tyr
 340 345 350
 Thr Asn Ala Pro Ala Tyr Leu Ile Glu Lys Glu Tyr Pro Leu Trp Arg
 355 360 365
 Ala Lys His Pro Thr Lys
 370

<210> 93

<211> 1062

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 93

gtggatccaa agaattggaa cccgaaaaaaaa gccgacgatt catggctcga aaagacgaaa

60

cccgattacc ggctggtctc ctggcgac	gttttagatc aaactcagct	ctggta	120
gtcgacgaag cgacgcgc	cat cgccaa	cagg	180
tggaaaaaa acgtcgacat	ggcg	cgatc	240
aaagaaaaat ctcacaccga	tacgaccatc	gacaacggcg	300
tatctggcaa aagtcatcac	ggcggaaa	ac atcga	360
ggattggatt ttctgctcg	gatcg	acttccgca	420
ttgaaaaaacg attattcg	cgagattact	ttcaacgacg	480
aaattgctgc	g	acgcatgat	540
cgcccccagag	cg	aatgattt	600
gcacatcgacg	gcaaa	tatcg	660
gcaaatgcga	gaaagt	ttcg	720
agattttga tgctcgacgc	caaaccgac	gaggaaaa	780
atcgaatgg	ttcaaaaa	tcggagcgat	840
aacctggtc	caaactgagc	ggcattcg	900
accatgcgcc	ccat	tttccggc	960
gaagccgaac gccgcaacgg	ctacggctgg	tacacgaacg	1020
aaagattatc	cgaaatggaa	agagaaaatt	1062

<210> 94
<211> 353
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(353)

<400> 94

Met	Asp	Pro	Lys	Asn	Trp	Asn	Pro	Lys	Lys	Ala	Asp	Asp	Ser	Trp	Leu
1					5			10						15	
Glu	Lys	Thr	Lys	Pro	Asp	Tyr	Arg	Leu	Val	Ser	Trp	Arg	Asp	Val	Leu
						20			25					30	
Asp	Gln	Thr	Gln	Leu	Trp	Tyr	Ala	Val	Asp	Glu	Ala	Thr	Arg	Ile	Ala
						35			40					45	
Asn	Gln	Val	Leu	Leu	Phe	Gln	Arg	Asp	Asn	Gly	Gly	Trp	Glu	Lys	Asn
						50			55					60	
Val	Asp	Met	Ala	Ala	Met	Leu	Thr	Gln	Ala	Glu	Arg	Glu	Lys	Leu	Val
						65			70					80	
Lys	Glu	Lys	Ser	His	Thr	Asp	Thr	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Thr
						85			90					95	
Thr	Gln	Leu	Arg	Tyr	Leu	Ala	Lys	Val	Ile	Thr	Ala	Lys	Asn	Ile	Glu
						100			105					110	
Ala	His	Lys	Gln	Ser	Phe	Leu	Lys	Gly	Leu	Asp	Phe	Leu	Leu	Ala	Met
						115			120					125	
Gln	Tyr	Glu	Asn	Gly	Gly	Phe	Pro	Gln	Tyr	Tyr	Pro	Leu	Lys	Asn	Asp
						130			135					140	
Tyr	Ser	Arg	Glu	Ile	Thr	Phe	Asn	Asp	Ala	Met	Ile	Asn	Val	Leu	
						145			150					160	
Lys	Leu	Leu	Arg	Asp	Val	Ala	Lys	Lys	Glu	Asp	Tyr	Leu	Phe	Val	
						165			170					175	
Asp	Glu	Asp	Arg	Arg	Ala	Arg	Ala	Glu	Gly	Ala	Val	Glu	Lys	Gly	Val
						180			185					190	
Arg	Leu	Ile	Leu	Lys	Thr	Gln	Val	Ala	Ile	Asp	Gly	Lys	Lys	Thr	Ile
						195			200					205	
Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Asn	Thr	Leu	Lys	Pro	Ala	Asn	Ala	Arg
						210			215					220	
Lys	Phe	Glu	Pro	Ala	Ser	Leu	Ala	Ser	Arg	Glu	Ser	Val	Ser	Val	Val

225	230	235	240
Arg Phe Leu Met Leu Asp Ala Lys Pro Asp	Glu Glu Lys Ile Gly Ala		
245	250	255	
Ile Glu Ser Ala Ile Glu Trp Phe Gln Lys Asn Lys Leu Ser Gly Ile			
260	265	270	
Arg Trp Glu Ser Lys Ser Gly Glu Asn Leu Val Val Lys Asp Lys Ala			
275	280	285	
Ala Pro Pro Ile Trp Gly Arg Phe Tyr Gln Phe Glu Thr Met Arg Pro			
290	295	300	
Ile Phe Ile Gly Arg Asp Ala Val Ile Arg Tyr Asp Val Met Gln Ile			
305	310	315	320
Glu Ala Glu Arg Arg Asn Gly Tyr Gly Trp Tyr Thr Asn Glu Pro Asn			
325	330	335	
Glu Leu Leu Asp Lys Asp Tyr Pro Lys Trp Lys Glu Lys Ile Lys Lys			
340	345	350	
Asn			

<210> 95
<211> 1074
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 95		
atgacgctac ccgtgtttc cctgcgcgtta ctgctggcgc tgctggccac gtcggccggc	60	
gcctgcgcgg ggcgcgcggc acccgcgact gcgaccgatc cggctgcgcga gaacatgctg	120	
cttctgcaga cccgcctccgg cggctggtcc aagcactacc gcgagaagaa ggtcgactac	180	
gcccgcgcact acgacgcgcg cggacgcgcg cgcgtgcgcg cgcgcgcgcg gcatgacgat	240	
gcaacatcgatcg acaacaaggc cacgaccacc gagatcgctt acctggtgc ggcacatgcc	300	
aggacgggca atccggccta cctcgacggc ggcgcgcgcg ggtcgagta cctgctgcgc	360	
gcccaggatcc cgaacggcgg ctggccgcga ttctaccccg accatcgatc ctaccggcac	420	
cagatcagtc tcaacgacga tgcgtatggtg cacgccatca cctgtgcgcg ggacatcgcc	480	
gccccggcga acggcatgca ggtgctggcg cggagttcg ggcgtccgcgc cggccggcc	540	
gcccggcgcc gcatcgaaaa cctgctcgag ttgcaggatgc gatcgccgg ggtggcgcacg	600	
atatggcccg cgcagtacga cggaccggc ctgcacccgg ccaaggcccg cgcgtacgaa	660	
ctgccttcgc tggccgtggc cgaatcggtc ggcgtgtgc gcctgtgtat ggcgcgcgcg	720	
gcccgtatcg cgcgcacggc cggccgcgc gaggccggcgg cggactggct ggaggcgcac	780	
cgcctgcggg acctcgccct ggaacgcac gaaaggcccg cggaggaaac cggcaaggac	840	
gtcccggtcg tggccagacc gggcgcgtcg ttgtggcgc gcttctacga cctcgagcgg	900	
caggtgccgc tggcgtcgatc tgcacacgc cgtccggcgc cttcgccga gcttcccaac	960	
gagcgtcgta cggctatgg ctggatggc acctggccgg aaaagctgt ggcacaggaa	1020	
ctccggcgct ggcgaaggc ccatgcggcc agcgcggcgc ctccggcccg ttga	1074	

<210> 96
<211> 357
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> DOMAIN
<222> (32)...(357)

<223> Catalytic domain

<400> 96
 Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
 1 5 10 15
 Thr Ser Pro Val Ala Cys Ala Gly Ala Ala Ala Pro Ala Thr Ala Thr
 20 25 30
 Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
 35 40 45
 Trp Ser Lys His Tyr Arg Glu Lys Lys Val Asp Tyr Ala Arg Asp Tyr
 50 55 60
 Asp Ala Ala Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg His Asp Asp
 65 70 75 80
 Ala Thr Ile Asp Asn Lys Ala Thr Thr Glu Ile Ala Tyr Leu Val
 85 90 95
 Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
 100 105 110
 Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
 115 120 125
 Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
 130 135 140
 Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
 145 150 155 160
 Ala Gly Arg Asn Gly Met Gln Val Leu Ala Pro Glu Phe Gly Val Arg
 165 170 175
 Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
 180 185 190
 Val Arg Ile Ala Gly Val Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
 195 200 205
 Thr Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
 210 215 220
 Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
 225 230 235 240
 Ala Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ala Ala Ala Asp Trp
 245 250 255
 Leu Glu Ala His Arg Leu Pro Asp Leu Ala Leu Glu Arg Ile Glu Ala
 260 265 270
 Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Ala Arg Pro Gly
 275 280 285
 Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Glu Arg Gln Val Pro Leu
 290 295 300
 Phe Val Asp Arg Asn Ser Arg Pro Val Pro Phe Ala Glu Leu Pro Asn
 305 310 315 320
 Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Gly Thr Trp Pro Glu Lys Leu
 325 330 335
 Leu Ala Gln Glu Leu Pro Arg Trp Arg Lys Val His Ala Ala Ser Ala
 340 345 350
 Gly Ala Pro Ala Arg
 355

<210> 97

<211> 2097

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 97

ttgaacgccc	ccggcagccg	gcggttcgcg	caactcgatcg	tcgcggatct	gcggcggtcg	60
gtgcccgcgc	tggccctt	cttcgcac	gagccgtcg	cgggaggagt	cgccgcgtc	120
cagcgacgc	tcgatgcgt	cgtcgcgcg	gacggcaccg	gacagttgc	gacggtgcag	180
gagggcgatca	acgcccgcgc	gcagaacacc	agcacgacca	gcccgtggat	catctcgatc	240
aaaccaggca	cgtatcgca	ggtcgtctac	gtgcagcgat	agaagcgctt	cgtcacgtcg	300
atcggcgaag	acccggcagc	gacgacgatc	acgtaccacc	tcaaagcgatc	tgacgtgggg	360
ctcgacggca	agcccatcg	cacgtttcg	acgcccacga	ttgtgttgg	tgccgacgat	420
ttcacgatcg	agaacccatc	catcgagaac	ggggcagggc	cggtcggtca	agcgctggcc	480
ttgcgagtgg	acggcgatcg	cgtgacgggt	aggaacagacc	gcctgtggg	ctggcaggac	540
acgatctttc	tcaaccgtgg	gcccactac	ttcgaggact	cgttcatcg	cggcacgtg	600
gatttcattt	tcggccggcgc	gacggcggtg	ttcgagcgat	gccatctcg	cgcctggcg	660
gacggctacc	tcacggccgc	gtccacgccc	gcccggcaac	gatcggttgc	cgtgttctg	720
aacagcatcg	tcagtggaga	agctggcgc	cgcaatcgat	tcgggtcgacc	gtggcggggcg	780
ttcgcgcacg	tggccttcat	caagacgacg	atggggcgagg	ttgtgtcgccc	gttgggctgg	840
aacaactgg	accggccgga	gctgtggaaag	accgtgcgtt	ttctcgaaac	aggcaccagc	900
ggcgcggggc	gcagcgatcg	tcgcgcgtc	gcctggggcgc	gggtcgccac	gccagccgag	960
ctcgctgatc	tgacgaccga	gggtgtgttgc	ggcggcaccg	acggctggga	cccgcgtcgc	1020
gtcgccccgt	acccgtcgcc	cgttcgcgc	aacggccgc	cgctgcgcg	gccgccccgg	1080
cccgacgtcg	ctggcccgca	gagccgcgc	gccttgcgt	gggaccaggt	cgcgcgcag	1140
ccagcgatcg	ggctggccac	acccgaagcg	ctgcggatttgc	ccgagaacgt	gacgccttat	1200
caacggcaca	ctggccgctg	gccccaaaac	ctcgacatgg	cgccggccgtt	gacgacgccc	1260
gatcgccgc	gtctcacggc	cgatcgccgc	ctcgacgact	cgaccatcg	caatggcgcc	1320
acgacgcggc	agatcgagtt	tctcgcccg	atcgccgcgc	ccaaccgcga	cgagcgccgc	1380
caggcgatcg	tgctggctgg	gatcgactac	ctgctcgccg	cccagatattc	aaacggccgc	1440
tgccgcagt	atttcccgt	ccgcaacgac	tactcgcc	acatcacgtt	caacgacgac	1500
gcatgatcg	cgccgcgcac	gatcctgc	tcgggtcgcc	tggcccggttcc	gccgttcgccc	1560
ggcgatcg	cgactcgccg	ccggcgccgc	gcccggccgc	tcggcgccgc	ccatcgctg	1620
attctggct	cgcagattcg	cgtcaacggc	cagctactg	gctggtgcca	gcagcacgt	1680
gcacgcacgc	tggagccagc	gcccggccgc	acctacgagc	atccatcgat	cagtgccgc	1740
gaaaccgtga	cgatcgtaa	tttcctgcgg	tcgatcgac	cgccgcgaccg	ccagacccaa	1800
gccgcacatcg	atcccgcat	ggagtggctc	aaggccgtgc	agatcccgccg	ctggcgacgc	1860
gagcgccggc	ccgatccctc	agagccgggc	ggttacgacg	ttgtgtatgtt	ggaggacccc	1920
aacgcggccgc	cgctctgggc	ccgcttctac	gagatggca	ccaatcgccc	gatctactcg	1980
ggccggggacg	gcgtcatcaa	gtacccgctc	gccgagatcg	aaattgaacg	gcggaccggc	2040
tacagctggg	tcggaccgta	cgcgcaggcg	ctgctcgatc	aagagcgacg	gaagtaa	2097

<210> 98

<211> 698

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (45)...(333)

<223> Pectin methyl esterase domain

<221> DOMAIN

<222> (336)...(698)

<223> Catalytic domain

<400> 98

Met Asn Ala Ala Gly Ser Arg Arg Phe Ala Gln Leu Val Val Ala Asp

1 5 10 15

Leu Arg Arg Leu Val Pro Ala Leu Ala Pro Phe Phe Arg Asp Glu Pro

20 25 30

Leu Ala Gly Gly Val Ala Ala Leu Gln Arg Ser Val Asp Ala Ile Val

35 40 45

Ala Ala Asp Gly Thr Gly Gln Phe Ala Thr Val Gln Glu Ala Ile Asn
 50 55 60
 Ala Ala Pro Gln Asn Thr Ser Thr Ser Arg Trp Ile Ile Leu Val
 65 70 75 80
 Lys Pro Gly Thr Tyr Arg Glu Val Val Tyr Val Gln Arg Glu Lys Arg
 85 90 95
 Phe Val Thr Leu Ile Gly Glu Asp Pro Ala Arg Thr Thr Ile Thr Tyr
 100 105 110
 His Leu Lys Ala Ser Asp Val Gly Leu Asp Gly Lys Pro Ile Gly Thr
 115 120 125
 Phe Arg Thr Pro Thr Met Val Val Asp Ala Asp Asp Phe Thr Ile Glu
 130 135 140
 Asn Leu Thr Ile Glu Asn Gly Ala Gly Pro Val Gly Gln Ala Leu Ala
 145 150 155 160
 Leu Arg Val Asp Gly Asp Arg Val Thr Val Arg Asn Ser Arg Leu Leu
 165 170 175
 Gly Trp Gln Asp Thr Ile Phe Leu Asn Arg Gly Arg His Tyr Phe Glu
 180 185 190
 Asp Ser Phe Ile Gly Gly His Val Asp Phe Ile Phe Gly Gly Ala Thr
 195 200 205
 Ala Val Phe Glu Arg Cys His Leu Arg Ala Trp Arg Asp Gly Tyr Leu
 210 215 220
 Thr Ala Ala Ser Thr Pro Ala Glu Gln Arg Phe Gly Phe Val Phe Leu
 225 230 235 240
 Asn Ser Ile Val Ser Gly Glu Ala Gly Ala Arg Thr Tyr Leu Gly Arg
 245 250 255
 Pro Trp Arg Ala Phe Ala His Val Ala Phe Ile Lys Thr Thr Met Gly
 260 265 270
 Glu Val Val Arg Pro Val Gly Trp Asn Asn Trp Asp Arg Pro Glu Arg
 275 280 285
 Glu Lys Thr Val Arg Phe Leu Glu Ala Gly Thr Ser Gly Ala Gly Gly
 290 295 300
 Ser Val Ala Ala Arg Val Ala Trp Ala Arg Val Ala Thr Pro Ala Glu
 305 310 315 320
 Leu Ala Asp Leu Thr Thr Glu Val Val Leu Gly Gly Thr Asp Gly Trp
 325 330 335
 Asp Pro Arg Arg Val Ala Pro Tyr Pro Ser Ala Val Arg Ala Asn Ala
 340 345 350
 Ala Pro Leu Pro Arg Pro Pro Gly Pro Asp Val Ala Gly Pro Gln Ser
 355 360 365
 Pro Pro Ala Leu Thr Trp Asp Gln Val Ala Arg Gln Pro Ala Ser Trp
 370 375 380
 Leu Ala Thr Pro Glu Ala Leu Arg Ile Ala Glu Asn Val Arg Leu Tyr
 385 390 395 400
 Gln Arg His Thr Gly Gly Trp Pro Lys Asn Leu Asp Met Ala Gln Pro
 405 410 415
 Leu Thr Asp Ala Asp Arg Ala Arg Leu Thr Ala Asp Arg Ala Leu Asp
 420 425 430
 Asp Ser Thr Ile Asp Asn Gly Ala Thr Thr Arg Gln Ile Glu Phe Leu
 435 440 445
 Ala Arg Ile Ala Ala Ala Asn Arg Asp Glu Arg Ala Gln Ala Ser Met
 450 455 460
 Leu Ala Gly Ile Asp Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly
 465 470 475 480
 Trp Pro Gln Tyr Phe Pro Leu Arg Asn Asp Tyr Ser Arg His Ile Thr
 485 490 495
 Phe Asn Asp Asp Ala Met Ile Ala Ala Ala Thr Ile Leu Gln Ser Val
 500 505 510
 Ala Leu Ala Arg Pro Pro Phe Ala Gly Val Asp Ala Thr Arg Arg Arg

515	520	525
Arg Ala Ala Glu Ala Val Ala Arg Ala His Arg Val Ile Leu Ala Ser		
530	535	540
Gln Ile Arg Val Asn Gly Gln Leu Thr Gly Trp Cys Gln Gln His Asp		
545	550	555
Ala Arg Thr Leu Glu Pro Ala Arg Gly Arg Thr Tyr Glu His Pro Ser		
565	570	575
Ile Ser Gly Arg Glu Thr Val Thr Ile Val Asn Phe Leu Arg Ser Ile		
580	585	590
Glu Pro Arg Asp Arg Gln Thr Gln Ala Ala Ile Asp Ala Ala Met Glu		
595	600	605
Trp Leu Lys Ala Val Gln Ile Arg Gly Trp Arg Thr Glu Arg Arg Pro		
610	615	620
Asp Pro Ser Gly Pro Gly Gly Tyr Asp Val Val Met Val Glu Asp Pro		
625	630	635
Asn Ala Ala Pro Leu Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg		
645	650	655
Pro Ile Tyr Ser Gly Arg Asp Gly Val Ile Lys Tyr Arg Leu Ala Glu		
660	665	670
Ile Glu Ile Glu Arg Arg Thr Gly Tyr Ser Trp Val Gly Pro Tyr Ala		
675	680	685
Gln Ala Leu Leu Asp Glu Glu Arg Arg Lys		
690	695	

<210> 99

<211> 1782

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 99

atgttcacta ctaacagctc tatttgcgcc	cgaaatccg cgcgttttc	actgactgcc	60
atggctgtcg cggtgctat gatcgccggc	acctctgcctt tgcggccctc	tacccgtggc	120
ttttcgacca cggatggcg	caatgtgtca gggtaaaaat	ccttaccgc ctcaagccac	180
acccaaatcc	agcaaatcc	tgaggatgcc aaagatggca	240
accacccggca	atgaggattc	attatccgtt ggtgatcacc	300
tcaggcaact	atgaggattc	caagtcgtcc gggatcacac	360
gccctaaagc	gcgttggat	cgatcgttacc gtttccatcc	420
atgaccaagg	gtgtcaccat	aatggttcgat	480
gtgaataaaat	ccagcaacgt	tttgcgttcc	540
aataacgatg	gattattcgc	aatatgttcc	600
ccgtatgtat	ccgtgtggac	ttttttttttt	660
gaattattcg	cgatgttaag	ttttttttttt	720
ccgtgaacaa	caacctgtac	ttttttttttt	780
agcgcgattt	atataaaaaa	ttttttttttt	840
gacagtaaaa	agcctcgcaa	ttttttttttt	900
atttgcgtt	gatatcaccg	ttttttttttt	960
tttgcgtt	ttttttttttt	ttttttttttt	1020
tttgcgtt	ttttttttttt	ttttttttttt	1080
tttgcgtt	ttttttttttt	ttttttttttt	1140
tttgcgtt	ttttttttttt	ttttttttttt	1200
tttgcgtt	ttttttttttt	ttttttttttt	1260
tttgcgtt	ttttttttttt	ttttttttttt	1320
tttgcgtt	ttttttttttt	ttttttttttt	1380
tttgcgtt	ttttttttttt	ttttttttttt	1440
tttgcgtt	ttttttttttt	ttttttttttt	1500
tttgcgtt	ttttttttttt	ttttttttttt	1560

ccgggtttaa gtggcacagg tgattaccca agccgttct ccaagtgtgc tgatctgggt	1620
ggcacctgct cagtcgcctc gggcgatggt tgggtgcct ttggtcgcaa aggcaagtgg	1680
gtcaccaaaa aagtgtcagt cggtagctct attgcctgta ccgttgccgc gtttggatct	1740
gatccacaag gcaatccaa taagtgttct tataaaaagt aa	1782

<210> 100
<211> 593
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(35)

<221> DOMAIN
<222> (36)...(593)
<223> Catalytic domain

<400> 100
Met Phe Thr Thr Asn Ser Ser Ile Cys Ala Arg Lys Ser Ala Arg Phe
1 5 10 15
Ser Leu Thr Ala Met Ala Ala Val Ala Met Ile Ala Gly Thr Ser
20 25 30
Ala Phe Ala Ala Ser Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
35 40 45
Val Ser Gly Ser Lys Ser Phe Thr Ala Ser Ser His Thr Gln Ile Gln
50 55 60
Gln Ile Leu Glu Asp Ala Lys Asp Gly Asn Tyr Pro Val Val Ile Thr
65 70 75 80
Tyr Thr Gly Asn Glu Asp Ser Leu Ile Asn Gln Val Val Arg Asp His
85 90 95
Thr Val Asp Ser Ser Gly Asn Cys Pro Lys Ala Arg Trp Asn Asp Ala
100 105 110
Tyr Arg Lys Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Gln
115 120 125
Gly Ala Asn Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser
130 135 140
Ser Asn Val Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Gly Gly Ala
145 150 155 160
Asn Asn Asp Ala Asp Met Ile Arg Val Asp Ser Gly Val Asn Val Trp
165 170 175
Ile Asp His Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser
180 185 190
Pro Asp Gly Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Ala
195 200 205
Ser Gln Asp Ile Thr Val Ser Tyr Asn Val Ile Arg Asp Ser Lys Lys
210 215 220
Val Gly Leu Asp Gly Ser Ser Ser Asp Ile Ala Gly Gly Arg Lys
225 230 235 240
Ile Thr Phe His His Asn Ile Tyr Arg Asn Val Gly Ala Arg Leu Pro
245 250 255
Leu Gln Arg Gly Gly Trp Thr His Met Tyr Asn Asn Leu Tyr Asp Gly
260 265 270
Ile Thr Ser Ser Gly Ile Asn Val Arg Gln Asn Gly Tyr Ala Leu Ile
275 280 285
Glu Ser Asn Trp Phe Gln Asn Ala Val Asn Pro Val Thr Cys Arg Phe
290 295 300

Asp Ser Ser Asn Cys Gly Lys Trp Asp Leu Arg Asn Asn Asn Ile Arg
 305 310 315 320
 Asn Pro Gly Asp Phe Ala Thr Tyr Asn Ile Thr Trp Thr Ser Gly Gly
 325 330 335
 Thr Ile Asp Ala Thr Asn Trp Thr Thr Ala Pro Phe Pro Ile Ser
 340 345 350
 Ile Pro Tyr Ser Tyr Ser Pro Val Thr Pro Gln Cys Val Lys Asp Arg
 355 360 365
 Leu Ala Ser Tyr Ala Gly Val Gly Lys Asn Gly Ala Gln Leu Thr Ala
 370 375 380
 Ser Ala Cys Gly Gly Ala Ala Ser Ser Thr Pro Ala Ser Ser Thr Pro
 385 390 395 400
 Ala Ser Ser Ser Ala Ala Asn Ser Ser Ala Ala Ser Gly Ser Val
 405 410 415
 Ser Leu Gly Gly Ser Ala Gly Asn Ala Ser Val Ala Leu Asn Trp Thr
 420 425 430
 Val Asn Ala Asn Ile Asn Ala Leu Glu Ile Tyr Gln Asp Thr Asp Ser
 435 440 445
 Asp Pro Ala Gly Arg Val Arg Ile Ala Ser Leu Pro Thr Ser Ala Thr
 450 455 460
 Asn Tyr Thr Ala Thr Gly Leu Ser Asn Gly Thr Tyr Tyr Phe Trp
 465 470 475 480
 Val Lys Tyr Arg Thr Thr Asn Asn Val Trp Ser Asn Ser Asn Val Phe
 485 490 495
 Ser Ala Lys Pro Ser Ser Gly Thr Thr Pro Ser Ser Ser Ser Ala
 500 505 510
 Ala Ser Ser Thr Pro Ser Gly Ala Pro Val Leu Ser Gly Thr Gly Asp
 515 520 525
 Tyr Pro Ser Gly Phe Ser Lys Cys Ala Asp Leu Gly Gly Thr Cys Ser
 530 535 540
 Val Ala Ser Gly Asp Gly Trp Val Ala Phe Gly Arg Lys Gly Lys Trp
 545 550 555 560
 Val Thr Lys Lys Val Ser Val Gly Ser Ser Ile Ala Cys Thr Val Ala
 565 570 575
 Ala Phe Gly Ser Asp Pro Gln Gly Asn Pro Asn Lys Cys Ser Tyr Lys
 580 585 590
 Lys

<210> 101

<211> 1404

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 101
 atgactatacgccgtcgagaattccttatagacccattatcgccaccgcggcattcgca
 atcgaccgcgtgtatcgcttccggcaagctatccatggaaaccgtctatccgaaatc
 ctcgctcgatcggccaccgaaatttccgaaagcgagatttcatcatcacatgttcggc
 gcaaagccggaaaccgcacgcggccgtcgatcgccaaatcgatcaccgcgtcagcaag
 gcaggcggagacgtgttctcggtccgcggagatgttttcacccggagcgtccatctg
 aaatcgaaacgtaaacttcaatgtcaaaaaatcgccgcgtggaaatttctcgaccgaccc
 aaggcatatctcccgattgtacatcgccatggaaatggatgtatcgatctgtca
 ccgttcatctacgcttatgacgacgaaatcgctatcaccggtcaggaaacgtcgac
 ggcagggaaatcatttcttctggaaatggcatggcaatccggcttatggcgcgatccg
 aacacgctcaatccacggcccgctcgatcgccgttacgagatgtatgatggataaagatgt
 ccggtcggccaaatgttcttcgtctcgatcattatctcgccggcgttgcgttattcagccg

tacaaatgca ggaacgtttt gatcgaagat	gtgacgatcg	tcgattcgcc	gatgtggaa	720
gttcatccgg	tgcttgcga	gaacgtcacg	gtccgaaatg	780
ccgaacaatg	acggatgcga	tccggagtcg	tgcaaggacg	840
ttcgacaccg	gcfgacattt	catcgcgatc	aagtccggcc	900
atcaatgtcc	cgaccgagaa	catcatcgatc	cgcaactgca	960
ggcatcacgg	tcggcagtga	gatttcggga	ggcgtgcgaa	1020
cgactcgaca	gtgcgatct	ctggaccgcg	cttcgcgtca	1080
ggcaagctcg	agaatttta	tttcggaat	ataacggtcg	1140
gtcgagatcg	atttaattt	cgaggaagggt	gcaaaaggct	1200
aattatgttg	ttgaaggact	gacatgcgcc	acaggcaatc	1260
ttggacaacg	cggcgcata	caatgttaacg	ctgcgaaact	1320
aatcgttagt	ttgtgaaaaaa	cgttcgttgg	gtacgtttgg	1380
agatcgtaa	acgaaactgg	cttcggctcg	agaatgtgaa	1404
acgaaactgg	atgaa	gatcggcgcc		

<210> 102

<211> 467

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(28)

<221> DOMAIN

<222> (78)...(459)

<223> Catalytic domain

<400> 102

Met	Thr	Ile	Asp	Arg	Arg	Glu	Phe	Leu	Ile	Asp	Leu	Ile	Ile	Gly	Thr
1						5				10					15
Ala	Gly	Phe	Ala	Ile	Ala	Pro	Ser	Asp	Ala	Phe	Gly	Gln	Ala	Asp	Pro
						20				25					30
Trp	Lys	Thr	Val	Tyr	Pro	Gln	Ile	Leu	Ala	Arg	Ile	Arg	Pro	Pro	Lys
						35				40					45
Phe	Pro	Lys	Arg	Asp	Phe	Ile	Ile	Thr	Arg	Phe	Gly	Ala	Lys	Pro	Gly
						50				55					60
Thr	Asp	Ser	Ala	Ala	Ala	Ile	Ala	Lys	Ala	Ile	Thr	Ala	Cys	Ser	Lys
						65				70					80
Ala	Gly	Gly	Arg	Val	Leu	Val	Pro	Ala	Gly	Glu	Phe	Leu	Thr	Gly	
						85				90					95
Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Phe	His	Val	Ser	Lys	Gly	Ala
						100				105					110
Thr	Leu	Lys	Phe	Ser	Thr	Asp	Pro	Lys	Ala	Tyr	Leu	Pro	Ile	Val	His
						115				120					125
Thr	Arg	Trp	Glu	Gly	Met	Glu	Leu	Met	His	Leu	Ser	Pro	Phe	Ile	Tyr
						130				135					140
Ala	Tyr	Glu	Gln	Thr	Asn	Ile	Ala	Ile	Thr	Gly	Gln	Gly	Thr	Leu	Asp
						145				150					160
Gly	Gln	Gly	Lys	Ser	Phe	Phe	Trp	Lys	Trp	His	Gly	Asn	Pro	Ala	Tyr
						165				170					175
Gly	Gly	Asp	Pro	Asn	Thr	Leu	Ser	Gln	Arg	Pro	Ala	Arg	Ala	Arg	Leu
						180				185					190
Tyr	Glu	Met	Met	Asp	Lys	Asn	Val	Pro	Val	Ala	Glu	Arg	Val	Phe	Gly
						195				200					205
Leu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro	Tyr	Lys	Cys	Arg
						210				215					220
Asn	Val	Leu	Ile	Glu	Asp	Val	Thr	Ile	Val	Asp	Ser	Pro	Met	Trp	Glu

225	230	235	240
Val His Pro Val Leu Cys Glu Asn Val Thr Val Arg Asn Val His Ile			
245	250	255	
Ser Ser His Gly Pro Asn Asn Asp Gly Cys Asp Pro Glu Ser Cys Lys			
260	265	270	
Asp Val Leu Ile Asp Asn Cys Phe Phe Asp Thr Gly Asp Asp Cys Ile			
275	280	285	
Ala Ile Lys Ser Gly Arg Asn Asn Asp Gly Arg Arg Ile Asn Val Pro			
290	295	300	
Thr Glu Asn Ile Ile Val Arg Asn Cys Thr Met Lys Asp Gly His Gly			
305	310	315	320
Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val Arg Asn Leu Phe			
325	330	335	
Ala His Asp Cys Arg Leu Asp Ser Ala Asp Leu Trp Thr Ala Leu Arg			
340	345	350	
Val Lys Asn Asn Ala Ser Arg Gly Gly Lys Leu Glu Asn Phe Tyr Phe			
355	360	365	
Arg Asn Ile Thr Val Gly Gln Val Ala Arg Ala Val Val Glu Ile Asp			
370	375	380	
Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Tyr Ile Pro Val Val Arg			
385	390	395	400
Asn Tyr Val Val Glu Gly Leu Thr Cys Ala Thr Gly Asn Arg Ala Val			
405	410	415	
Asp Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asn Val Thr Leu Arg			
420	425	430	
Asn Cys Thr Phe Gly Ser Val Arg Asn Arg Ser Val Val Lys Asn Val			
435	440	445	
Arg Gly Leu Arg Leu Glu Asn Val Lys Ile Gly Gly Arg Ile Val Asn			
450	455	460	
Glu Leu Val			
465			

<210> 103

<211> 1101

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 103

atgaacaccg cactgcaccg cgtcatccgc ctgcccgtgc tgctggcgct gtgcctgccc	60
gcgcgtcagg cacaggccac gcagaccgag cccgtcgccg agaacatgt gctgtgcag	120
accgcgtccg gcggctggtc caagcaccac cagggcaagg cggtcgacta cggccacacg	180
ttcacccatg ccgaacgtgc ggcgtcgcc gcgcggacc gcagggacga tgcgacgatc	240
gacaacaagg cgaccacgt tgagatcgtc ggcgtctgg aagccacca ggcgcaccggc	300
aatgcgcct atctggcggc tgccgacgc ggcgtggact acctgctgca cgcgcagtac	360
ccgaacggcg gctggccgca gtactaccg gaccgttcgc tgcgtggcgtt ccaggtcacc	420
ttcaacatg atgcgtatgac ccgcgtgctg gagctgtgc aggacatgt cgagggcaag	480
ggcgcgtctgg cgcaatgtac accccacgcgt ggcgaacgcg ccaggccgc gctcgacagg	540
ggcatcgccct gcgtgtcgcc cacccaggta cggatcgatg gcgagctcac gctctggcc	600
gcgcagtacg acgaagccac gctgcagccg gcaaggccgc gctcctacga gctccatcg	660
ctggcggtcg ccgaatcggt cgggggtgtatg cggctgtca tgccgcaggcc acagccgtcg	720
ccgcagggtgc tgacggcggt cgaggccggc gcacgtggc tggaggccca ccgcgtcgcc	780
gacctggccc ggcgaaagat cgacgcgccc ggcgaagaaa ccggccaggaa cgtggtgatc	840
gtcgccgagc cggcgccgtc gctgtggca cgcttctacg acctgcagaca ccagcagccg	900
atgttcgtga accgcgaagg cgagcaggta gcccgttgc cgcacatgcc caacgaacgc	960
cgcgctcggtc acgcctggta tggcggtgtgg ccggagaagc tgctgcagaca ggagctgcca	1020
cgctggtaca acaccatgc cgaggcattg cgcgcgattt cgccgtcgca tgccgagcca	1080

aggccgcccga agcggccctg a

1101

<210> 104

<211> 366

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(26)

<221> DOMAIN

<222> (27)...(366)

<223> Catalytic domain

<400> 104

Met	Asn	Thr	Ala	Leu	His	Arg	Val	Ile	Arg	Leu	Pro	Leu	Leu	Leu	Ala
1				5				10						15	
Leu	Cys	Leu	Pro	Ala	Leu	Gln	Ala	Gln	Ala	Thr	Gln	Thr	Glu	Pro	Val
				20				25						30	
Ala	Glu	Asn	Met	Leu	Leu	Leu	Gln	Thr	Ala	Ser	Gly	Gly	Trp	Ser	Lys
	35				40				45						
His	His	Gln	Gly	Lys	Ala	Val	Asp	Tyr	Gly	His	Thr	Phe	Thr	Asp	Ala
	50				55			60							
Glu	Arg	Ala	Ala	Leu	Arg	Ala	Pro	Asp	Arg	Arg	Asp	Asp	Ala	Thr	Ile
	65				70			75						80	
Asp	Asn	Lys	Ala	Thr	Thr	Leu	Glu	Ile	Val	Ala	Leu	Leu	Glu	Ala	His
				85			90							95	
Gln	Arg	Thr	Gly	Asn	Ala	Ala	Tyr	Leu	Ala	Ala	Ala	Gln	Arg	Gly	Val
	100				105			110							
Asp	Tyr	Leu	Leu	Ala	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr
	115				120			125							
Tyr	Pro	Asp	Arg	Ser	Leu	Tyr	Arg	His	Gln	Val	Thr	Phe	Asn	Asp	Asp
	130				135			140							
Ala	Met	Thr	Arg	Val	Leu	Glu	Leu	Leu	Gln	Asp	Ile	Val	Glu	Gly	Lys
	145				150			155						160	
Gly	Ala	Leu	Ala	Gln	Leu	Thr	Pro	Thr	His	Gly	Glu	Arg	Ala	Arg	Ala
				165			170						175		
Ala	Leu	Asp	Arg	Gly	Ile	Ala	Cys	Val	Leu	Ala	Thr	Gln	Val	Arg	Ile
		180			185			190							
Asp	Gly	Glu	Leu	Thr	Leu	Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Ala	Thr	Leu
	195				200			205							
Gln	Pro	Ala	Lys	Ala	Arg	Ser	Tyr	Glu	Leu	Pro	Ser	Leu	Ala	Val	Ala
	210				215			220							
Glu	Ser	Val	Gly	Val	Met	Arg	Leu	Leu	Met	Arg	Gln	Pro	Gln	Pro	Ser
	225				230			235						240	
Pro	Gln	Val	Leu	Thr	Ala	Val	Glu	Ala	Gly	Ala	Arg	Trp	Leu	Glu	Ala
				245			250						255		
His	Arg	Met	Arg	Asp	Leu	Ala	Arg	Arg	Lys	Ile	Asp	Ala	Pro	Gly	Glu
		260			265			270							
Glu	Thr	Gly	Gln	Asp	Val	Val	Ile	Val	Ala	Glu	Pro	Gly	Ala	Ser	Leu
		275			280			285							
Trp	Ala	Arg	Phe	Tyr	Asp	Leu	Gln	His	Gln	Gln	Pro	Met	Phe	Val	Asn
	290				295			300							
Arg	Glu	Gly	Glu	Gln	Val	Ala	Arg	Phe	Ala	Asp	Met	Pro	Asn	Glu	Arg
	305				310			315						320	
Arg	Val	Gly	Tyr	Ala	Trp	Tyr	Gly	Val	Trp	Pro	Glu	Lys	Leu	Leu	Gln

325	330	335
Gln Glu Leu Pro Arg Trp Tyr Asn Thr His Ala Glu Ala Leu Arg Ala		
340	345	350
Ile Thr Pro Ala His Ala Glu Pro Arg Pro Pro Lys Arg Pro		
355	360	365

<210> 105
<211> 1203
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 105		
atgcaattca tcgaaacaca gcaattgggg accgcgcgca aaccgtggc gggacgagga	60	
ggcgcacaggc gcttcccgcg ggtcatgccc gccgttgcg cgggccttgc ctcgcgcgt	120	
tcgtcggccg agccggcccg ggcgcaggcc gccggatgcgg atgcggatgg cccactgccc	180	
aggtgttggaca ggaggctgggt ggtatgcggcc gaggactggc tcgcctccggc cgaggacag	240	
cgcgttgcgg ccaacgtcct ccgctaccaa tcggcggaaag gagcctggc caaaaacacc	300	
aatctggccg ccactccct tcgcccccgag gacattccct ctcgcaccc cgggtggcc	360	
aacacgatcg acaatgaagc caccaccgtg cccattcggt tttggcccg ttcgcgcaa	420	
atcaacgagg acacggccag ccgcgaggcc gtcgcggc gattggacta ttcgcgtcaag	480	
gcgcataatc cgaacgttgg ctggccggcag tatttccgc tccgcccgcg ctaccactg	540	
cacatcacct acaacgacca cccatggtg aatgtgtcg acctgtctgc ggacgtgtcg	600	
ctgggcgagg agccgttgcgat tttgtggac gaggatcgcc gccagcggcc cgacgcgc	660	
gtggagcggg ggatcgaaatcg catcctccgc acccaaattcc ggcaggagga ccaacccacc	720	
ggctgggtgcg cgcagttatcg ccccgaaacc ttggcccccgg cgtggggacg ggcgtacgag	780	
ccggccgtcga tttccggcgcg cggacccgtc ggcgtggcgc ggtttctgat ggcgtggag	840	
tcgcctcgcg cggaaaggccgt cgaagccatc gagggccca tcgcctggct cgacacggcg	900	
ggcatcgagg aattgcgtct cgaatggttc accaacagcg agggcaagcg tgaccggcgc	960	
gtggtcgagg acgcttccgt gggcacctt tgggcgcgt tttacgaact cgaaacgaac	1020	
cgccccctgt tcgtggaccg cgacgggttg ctccgcgtacttcgacttcgcgacttcgcg	1080	
gagcggccgc aaggttacag ctactacggc acttggccgg cgccattgttgc ggccacggaa	1140	
tatccgcgtt ggcgcaggat gaacgagtcc gcccgtctcg agtcgtcctt catctcgcat	1200	
tga	1203	

<210> 106
<211> 400
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(43)

<221> DOMAIN
<222> (44)...(400)
<223> Catalytic domain

<400> 106		
Met Gln Phe Ile Glu Thr Gln Gln Leu Gly Thr Ala Ala Lys Pro Val		
1 5 10 15		
Ala Gly Arg Gly Gly Asp Arg Arg Phe Pro Arg Val Met Pro Ala Val		
20 25 30		
Cys Ala Gly Leu Ala Leu Ala Val Ser Ser Ala Glu Pro Val Arg Ala		
35 40 45		

Gln Gly Ala Asp Ala Asp Ala Asp Gly Pro Leu Pro Arg Trp Asn Arg
 50 55 60
 Arg Leu Val Asp Arg Pro Glu Asp Trp Phe Ala Ser Asp Glu Gly Gln
 65 70 75 80
 Arg Val Ala Ala Asn Val Leu Arg Tyr Gln Ser Ala Glu Gly Ala Trp
 85 90 95
 Pro Lys Asn Thr Asn Leu Ala Ala Thr Pro Leu Arg Pro Glu Asp Ile
 100 105 110
 Pro Ser Ser Thr Ser Gly Val Ala Asn Thr Ile Asp Asn Glu Ala Thr
 115 120 125
 Thr Val Pro Ile Arg Phe Leu Ala Arg Phe Ala Gln Ile Asn Glu Asp
 130 135 140
 Thr Ala Ser Arg Glu Ala Val Gln Arg Gly Leu Asp Tyr Leu Leu Lys
 145 150 155 160
 Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Tyr Phe Pro Leu Arg Arg
 165 170 175
 Gly Tyr His Ser His Ile Thr Tyr Asn Asp Asp Ala Met Val Asn Val
 180 185 190
 Leu Asp Leu Leu Asp Val Ser Leu Gly Glu Glu Pro Phe Asp Phe
 195 200 205
 Val Asp Glu Asp Arg Arg Gln Arg Ala Ala Thr Ala Val Glu Arg Gly
 210 215 220
 Ile Glu Cys Ile Leu Arg Thr Gln Ile Arg Gln Glu Asp Gln Pro Thr
 225 230 235 240
 Gly Trp Cys Ala Gln Tyr Asp Pro Glu Thr Leu Ala Pro Ala Trp Gly
 245 250 255
 Arg Ala Tyr Glu Pro Pro Ser Ile Ser Gly Ala Glu Thr Val Gly Val
 260 265 270
 Ala Arg Phe Leu Met Arg Leu Glu Ser Pro Ser Pro Glu Ala Val Glu
 275 280 285
 Ala Ile Glu Gly Ala Ile Ala Trp Leu Asp Thr Val Gly Ile Glu Glu
 290 295 300
 Leu Arg Leu Glu Trp Phe Thr Asn Ser Glu Gly Lys Arg Asp Arg Arg
 305 310 315 320
 Val Val Glu Asp Ala Ser Val Gly Thr Leu Trp Ala Arg Phe Tyr Glu
 325 330 335
 Leu Glu Thr Asn Arg Pro Leu Phe Val Asp Arg Asp Gly Val Leu Arg
 340 345 350
 Tyr Asp Phe Ala Glu Leu Thr Ala Glu Arg Arg Gln Gly Tyr Ser Tyr
 355 360 365
 Tyr Gly Thr Trp Pro Ala Pro Leu Leu Ala Thr Glu Tyr Pro Arg Trp
 370 375 380
 Arg Arg Met Asn Glu Ser Ala Leu Leu Glu Ser Ser Phe Ile Ser His
 385 390 395 400

<210> 107

<211> 1074

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 107

atgacgctac ccgttgttcc cctgcgcgtta ctgctggcgc tgctggccac gtcggccggc	60
gcctgcgcgg gcgctgcggc acccgcgact gcgaccgatc cggtcgcggaa gaacatgctg	120
cttctgcaga ccgcctccgg cggctggtcc aagcactacc gcgagaagaa ggtcgactac	180
gcgcgact acgacgcccgc cgagcgcgcgc ggcgtgcgcg cgccccgaccg gcatgacgat	240
gccacgatcg acaacaaggc caccgaccacc gagatcgcat acctggtgca ggcacatgcc	300

aggacgggca	atccggccta	cctcgacggc	gcgcgcccgcg	gcgtcgagta	cctgctgcgc	360
gcgcagtacc	cgaacggcgg	ctggccgcag	ttctaccccg	accattcgctc	ctaccggcac	420
cagatcacgc	tcaacgacga	tgcgatggtg	cacgcacatca	ccgtgctgca	ggacatcgcc	480
gcggggccgca	acggcatgca	ggtgtctggc	ccggagttcg	gcgtccgcgc	cgccggggcc	540
gcgcagcgcg	gcatcgaaaa	cctgctcgag	ttgcaggtgc	ggatcgacgg	gtgcccggacg	600
atctggcccg	cgcagtacga	cgagaccacc	ctgcaaccgg	ccaaggcccc	tgcgtacgag	660
ttgcccctcgc	tggccgtggc	cgaatcggtg	ggcgtgatgc	gcctgctgat	gcgcagcgg	720
gggcctgtatg	cgcgcacgat	cgccgcgatc	gaggccgcgg	cggactggct	ggaggccgac	780
cgcctgcccgg	acctcgccct	ggaacgcatac	gaagcccccg	ccgaggaaac	cgcaaggac	840
gtccgcgtcg	tggccagacc	gggcgcgtcg	ttgtgggcgc	gcttctacgta	cctcgagcgg	900
caggtgccgc	tgttcgtcga	tcgcaacacgc	cgtccggttc	cattcgccga	gcttcccaac	960
gaggctcgta	ccggctatgg	ctggtatggc	acctggccgg	aaaagctgct	ggcacaggaa	1020
ctcccgcgct	ggcgcaaggt	ccatgcggcc	agcgcggcgg	ctccggcccc	ttga	1074

<210> 108

<211> 357

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(31)

<221> DOMAIN

<222> (32)...(357)

<223> Catalytic domain

<400> 108

Met	Thr	Leu	Pro	Val	Val	Ser	Leu	Arg	Val	Leu	Leu	Ala	Leu	Leu	Ala
1				5					10			15			
Thr	Ser	Pro	Val	Ala	Cys	Ala	Gly	Ala	Ala	Ala	Pro	Ala	Thr	Ala	Thr
					20				25			30			
Asp	Pro	Val	Ala	Glu	Asn	Met	Leu	Leu	Leu	Gln	Thr	Ala	Ser	Gly	Gly
					35				40			45			
Trp	Ser	Lys	His	Tyr	Arg	Glu	Lys	Lys	Val	Asp	Tyr	Ala	Arg	Asp	Tyr
					50				55			60			
Asp	Ala	Ala	Glu	Arg	Ala	Ala	Leu	Arg	Ala	Pro	Asp	Arg	His	Asp	Asp
					65				70			75			80
Ala	Thr	Ile	Asp	Asn	Lys	Ala	Thr	Thr	Thr	Glu	Ile	Ala	Tyr	Leu	Val
					85				90			95			
Gln	Ala	His	Ala	Arg	Thr	Gly	Asn	Pro	Ala	Tyr	Leu	Asp	Gly	Ala	Arg
					100				105			110			
Arg	Gly	Val	Glu	Tyr	Leu	Leu	Arg	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp
					115				120			125			
Pro	Gln	Phe	Tyr	Pro	Asp	His	Ser	Ser	Tyr	Arg	His	Gln	Ile	Thr	Leu
					130				135			140			
Asn	Asp	Asp	Ala	Met	Val	His	Ala	Ile	Thr	Val	Leu	Gln	Asp	Ile	Ala
					145				150			155			160
Ala	Gly	Arg	Asn	Gly	Met	Gln	Val	Leu	Ala	Pro	Glu	Phe	Gly	Val	Arg
					165				170			175			
Ala	Ala	Ala	Ala	Gln	Arg	Gly	Ile	Gly	Asn	Leu	Leu	Glu	Leu	Gln	
					180				185			190			
Val	Arg	Ile	Asp	Gly	Val	Pro	Thr	Ile	Trp	Ala	Ala	Gln	Tyr	Asp	Glu
					195				200			205			
Thr	Thr	Leu	Gln	Pro	Ala	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Pro	Ser	Leu
					210				215			220			
Ala	Val	Ala	Glu	Ser	Val	Gly	Val	Met	Arg	Leu	Leu	Met	Arg	Gln	Pro

225	230	235	240
Gly Pro Asp Ala Arg Thr Ile Ala Ala Ile	Glu Ala Ala Ala Asp Trp		
245	250	255	
Leu Glu Ala His Arg Leu Pro Asp	Leu Ala Leu Glu Arg Ile Glu Ala		
260	265	270	
Pro Ala Glu Glu Thr Gly Lys Asp	Val Arg Val Val Ala Arg Pro Gly		
275	280	285	
Ala Ser Leu Trp Ala Arg Phe Tyr Asp	Leu Glu Arg Gln Val Pro Leu		
290	295	300	
Phe Val Asp Arg Asn Ser Arg Pro Val Pro	Phe Ala Glu Leu Pro Asn		
305	310	315	320
Glu Arg Arg Thr Gly Tyr Gly Trp Tyr	Gly Thr Trp Pro Glu Lys Leu		
325	330	335	
Leu Ala Gln Glu Leu Pro Arg Trp Arg	Lys Val His Ala Ala Ser Ala		
340	345	350	
Gly Ala Pro Ala Arg			
355			

<210> 109

<211> 1422

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 109

atgacgacac gacgccaatt catcaaaggc	tttctactta ccggagcagc	cgtggccgtc	60
gctcccggtt tgcttcgtt cgcccgaggag	gcaagtccgt	ggaaacgat gatgccttcg	120
atccctcgac gcatacggacc acctcggttt	ccgaaacgca	ctttctatct caatcgattc	180
ggcgccaaagg gtgtatggagt	cacagactgc	accgcggctt ttcatcgccg	240
tgcaccaaaag ccggccgtgg	gaaagtctgc	gtgcggccgg	300
attcatttga agagcaacgt	caacctcgaa	gacttatact caccggcg	360
caggacccga aacactacct	gtctcgaaag	gcgcgacgat caagttcagt	420
aactactcgc	tttcattta	ggaaagggtgt	480
cggatgtgg agattcatcc	cgcgttcgaa	cgaagtcttc	540
acgctcgacg gacagagtga	tgcggAACAC	tcgcgtac	600
ggatggaaag aaggatgaa	ttgtggccgt	ggAACGGCCG	660
gagaaaggcg	ggatggaaag	tcccgactac	720
ttcatttcgc	tttggcgaag	cgatccagg	780
ccgatgtgg	gtcatttgc	gctgtacgt	840
gatagtcatg	cgatccatcg	ctattcacga	900
aaggatagct	tttgcgtac	cgatccatcg	960
acatcgatc	tttgcgtac	ttcaaggatg	1020
gacggccgc	tttgcgtac	tcgcgtac	1080
ggcttaaaggc	tttgcgtac	tttgcgtac	1140
gacggccacg	tttgcgtac	tttgcgtac	1200
gtggaatcac	tttgcgtac	tttgcgtac	1260
gccgagaatt	tttgcgtac	tttgcgtac	1320
gcccattgtcg	tttgcgtac	tttgcgtac	1380
gcccattgtcg	tttgcgtac	tttgcgtac	1422

<210> 110

<211> 474

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (28)...(308)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (309)...(637)
 <223> Catalytic domain

<400> 110

Met	Thr	Thr	Arg	Arg	Glu	Phe	Ile	Lys	Gly	Phe	Leu	Leu	Thr	Gly	Ala
1					5			10					15		
Ala	Val	Ala	Val	Ala	Pro	Arg	Leu	Leu	Ala	Phe	Ala	Ala	Glu	Ala	Ser
					20			25					30		
Pro	Trp	Glu	Thr	Met	Met	Pro	Ser	Ile	Leu	Ala	Arg	Ile	Arg	Pro	Pro
					35			40			45				
Arg	Phe	Pro	Lys	Arg	Thr	Phe	Tyr	Leu	Asn	Arg	Phe	Gly	Ala	Lys	Gly
					50			55			60				
Asp	Gly	Val	Thr	Asp	Cys	Thr	Ala	Ala	Phe	His	Arg	Ala	Ile	Asp	Glu
					65			70		75			80		
Cys	Thr	Lys	Ala	Gly	Gly	Gly	Lys	Val	Val	Val	Pro	Ala	Gly	Thr	Tyr
					85			90			95				
Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Leu	Glu	Val	Ser
					100			105			110				
Glu	Gly	Ala	Thr	Ile	Lys	Phe	Ser	Gln	Asp	Pro	Lys	His	Tyr	Leu	Pro
					115			120			125				
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser	Pro
					130			135			140				
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Arg	Asn	Ile	Ala	Ile	Thr	Gly	Lys	Gly
					145			150			155			160	
Thr	Leu	Asp	Gly	Gln	Ser	Asp	Ser	Glu	His	Trp	Trp	Pro	Trp	Asn	Gly
					165			170			175				
Arg	Pro	Gln	Tyr	Gly	Trp	Lys	Glu	Gly	Met	Lys	Gln	Gln	Arg	Pro	Asp
					180			185			190				
Arg	Asn	Ala	Leu	Phe	Thr	Met	Ala	Glu	Lys	Gly	Val	Pro	Val	Arg	Glu
					195			200			205				
Arg	Ile	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro
					210			215			220				
Tyr	Arg	Cys	Gln	Asn	Val	Leu	Ile	Gln	Gly	Val	Thr	Ile	Arg	Asn	Ser
					225			230			235			240	
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Thr	Ile	His
					245			250			255				
Asp	Val	His	Ile	Asp	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn	Pro
					260			265			270				
Glu	Ser	Cys	Ser	Asp	Val	Leu	Ile	Lys	Asp	Ser	Tyr	Phe	Asp	Thr	Gly
					275			280			285				
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg	Arg
					290			295			300				
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Ile	Ile	Val	Gln	Gly	Cys	Arg	Met	Lys
					305			310			315			320	
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val
					325			330			335				
Arg	Asn	Leu	Phe	Ala	Glu	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu	Asp
					340			345			350				
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu	Glu
					355			360			365				

Asn	Phe	His	Phe	Arg	Asn	Ile	Glu	Val	Gly	Gln	Val	Ala	His	Ala	Val
370						375					380				
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe	Thr
385						390				395				400	
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Arg	Leu	Arg	Ser	Thr	Lys	Ser
						405			410				415		
Lys	His	Ala	Leu	Asp	Val	Gln	Gly	Leu	Pro	Gly	Ala	Pro	Val	Ile	Asn
						420		425			430				
Leu	Arg	Leu	Thr	Asn	Cys	Thr	Phe	Asn	Asp	Val	Gln	Gln	Pro	Asn	Ile
						435		440			445				
Leu	Lys	Asn	Val	Glu	Gln	Ser	Thr	Phe	Glu	Asn	Val	Thr	Ile	Asn	Gly
						450		455			460				
Lys	Thr	Ile	Thr	Gln	Thr	Gly	Ser	Lys	Glu						
						465		470							

<210> 111

<211> 1440

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 111

atgcaaaatc	gtcgagaatt	tttacaactt	ttatggccg	gtgcccgtgc	cggaacttgg		60
ttgccgcaga	tttcttcgg	gcagactaaa	caagccgacg	cctggacgac	cgagtatccg		120
aagattttag	ccagaatcaa	accgcccggaa	tttcgcaaaa	aagattttcc	gatcaccaaa		180
tatggagccg	ttgcggacgg	aaaaaccctg	gcgaccgaaa	gcatcaaaaa	agccatcgaa		240
gcgtgcgcca	aatcggccgg	cgggcgcg	gtcgtgcccc	agggagaatt	tttgaccggc		300
gcgattcatt	tgaaatcaa	cgtcaatctg	cacatcacga	aaggcgcgac	cgtcaaattt		360
tccaccaacc	cgaaagatta	tctgcccgtc	gttcacacgc	gctggaaagg	gatgaaattt		420
atgcataattt	cgccttaat	ttatgcctac	gagcaaacca	acatcgccgt	caccggcgag		480
ggaacgctcg	acgggcaggg	caaggctttt	ttctggaaat	ggcacggaaa	cccgcgctac		540
ggcgaaatc	cggatgtgat	cagccagcg	ccggcgcg	ccggctgt	tgaatgtat		600
gaaaaaggcg	tgcctgtgc	ggagcggatt	ttcggcgaaa	ctcagtatct	tcgcccgcag		660
tttatccagc	cctataaaatg	caaaaatgtt	ttgatcgaag	gcgttaaaat	catcgattcg		720
ccgatgtggg	aagttcaccc	cgttttgtgc	aaaaacgtga	cgatccgaaa	acttcatatt		780
tctacccacg	gaccgaacaa	cgacgggtgc	gatccggaaa	gctgcaagga	cgttttgtat		840
gaagactgct	atttcgacac	cggcgacgt	tgcattgcca	tcaaggcggg	gcbcataatgaa		900
gacgggcgac	gcatcaatgt	tccgaccgaa	aacgtcg	tgcgcgggtg	cgtgatgaaag		960
gacggtcacg	gcgaaatcac	catcggaagc	gagattccg	gcggcgtgc	aaatgtttc		1020
gcgaaaaca	accggctcg	cagcgcggat	ttgtggactg	cgctgagat	aaaaaacaac		1080
gcttcgcgcg	gcggaaaact	ggagaatttt	tacttccgc	atatcaccgt	cgggcagg		1140
tcgcgcgcgg	tcgtcgaaat	agattttat	tacgaggaag	gcgctaaagg	aaaacacacg		1200
ccggcgttc	gcaattacgt	ggtcggaaat	ctaacctgca	ataaaggcaa	tcgagcgg		1260
gatctgcagg	gcttggacaa	cgccccgatt	tacgacatca	cgatgaaaaa	ctgtacgttt		1320
aacgtggtcg	aaaagccgag	cgtcgtaaa	aacgtcaaag	gcgtcaaact	ggaaaacgtg		1380
aagattaacg	gcaaagtctg	cgagagtctg	gaaaatgctg	caacgacg	taaaaaataaa		1440

<210> 112

<211> 479

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1) ... (27)

<221> DOMAIN
 <222> (82)...(461)
 <223> Catalytic domain

<400> 112
 Met Gln Asn Arg Arg Glu Phe Leu Gln Leu Leu Phe Ala Gly Ala Gly
 1 5 10 15
 Ala Gly Leu Val Leu Pro Gln Ile Ser Phe Gly Gln Thr Lys Gln Ala
 20 25 30
 Asp Ala Trp Thr Thr Glu Tyr Pro Lys Ile Leu Ala Arg Ile Lys Pro
 35 40 45
 Pro Lys Phe Arg Lys Lys Asp Phe Pro Ile Thr Lys Tyr Gly Ala Val
 50 55 60
 Ala Asp Gly Lys Thr Leu Ala Thr Glu Ser Ile Lys Lys Ala Ile Glu
 65 70 75 80
 Ala Cys Ala Lys Ser Gly Gly Arg Val Val Val Pro Gln Gly Glu
 85 90 95
 Phe Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu His Ile
 100 105 110
 Thr Lys Gly Ala Thr Val Lys Phe Ser Thr Asn Pro Lys Asp Tyr Leu
 115 120 125
 Pro Ile Val His Thr Arg Trp Glu Gly Met Glu Leu Met His Ile Ser
 130 135 140
 Pro Leu Ile Tyr Ala Tyr Glu Gln Thr Asn Ile Ala Val Thr Gly Glu
 145 150 155 160
 Gly Thr Leu Asp Gly Gln Gly Lys Ala Phe Phe Trp Lys Trp His Gly
 165 170 175
 Asn Pro Arg Tyr Gly Gly Asn Pro Asp Val Ile Ser Gln Arg Pro Ala
 180 185 190
 Arg Ala Arg Leu Tyr Glu Met Met Glu Lys Gly Val Pro Val Ala Glu
 195 200 205
 Arg Ile Phe Gly Glu Thr Gln Tyr Leu Arg Pro Gln Phe Ile Gln Pro
 210 215 220
 Tyr Lys Cys Lys Asn Val Leu Ile Glu Gly Val Lys Ile Ile Asp Ser
 225 230 235 240
 Pro Met Trp Glu Val His Pro Val Leu Cys Glu Asn Val Thr Ile Arg
 245 250 255
 Lys Leu His Ile Ser Thr His Gly Pro Asn Asn Asp Gly Cys Asp Pro
 260 265 270
 Glu Ser Cys Lys Asp Val Leu Ile Glu Asp Cys Tyr Phe Asp Thr Gly
 275 280 285
 Asp Asp Cys Ile Ala Ile Lys Ala Gly Arg Asn Glu Asp Gly Arg Arg
 290 295 300
 Ile Asn Val Pro Thr Glu Asn Val Val Val Arg Gly Cys Val Met Lys
 305 310 315 320
 Asp Gly His Gly Ile Thr Ile Gly Ser Glu Ile Ser Gly Gly Val
 325 330 335
 Arg Asn Val Phe Ala Glu Asn Asn Arg Leu Asp Ser Ala Asp Leu Trp
 340 345 350
 Thr Ala Leu Arg Val Lys Asn Asn Ala Ser Arg Gly Gly Lys Leu Glu
 355 360 365
 Asn Phe Tyr Phe Arg Asp Ile Thr Val Gly Gln Val Ser Arg Ala Val
 370 375 380
 Val Glu Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Lys His Thr
 385 390 395 400
 Pro Val Val Arg Asn Tyr Val Val Glu Asn Leu Thr Cys Asn Lys Gly
 405 410 415
 Asn Arg Ala Val Asp Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asp

420	425	430
Ile Thr Met Lys Asn Cys Thr Phe Asn Val Val Glu Lys Pro Ser Val		
435	440	445
Val Lys Asn Val Lys Gly Val Lys Leu Glu Asn Val Lys Ile Asn Gly		
450	455	460
Lys Val Val Glu Ser Leu Glu Asn Ala Ala Thr Thr Ala Lys Lys		
465	470	475

<210> 113

<211> 1017

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 113

atgaagat ttttaacaat attgctctcg gcattattca gcatttcaaa tgcacaggtg	60
ctatcggttc ctgttgcgga tcgtatgacc agctaccaac ttaaaaacgg aggctggccg	120
aaggacttgg ccgataaaatc tgttgttaac tattcaaaaac ctctctcacc tgcttgcaa	180
aaagtcatcg atcaatcgac cgaaaaagtct ggcacaattg ataataatgc aaccacacgt	240
gagataaaacc atcttctcct cgcttattcc aaaaccaaca atgacaaga tcttcaagcg	300
gcgcacaaaag gtgtttagt tattcttgagt gctcaaaatg acaaaggagg atggctcaa	360
tattatccag acagtagctc atatcggtt cagatcacct acaatgacgg cgcatgatt	420
aatgtattgg aaattttact ttccatatac acaaacaag agccctatgc tggcttaacg	480
aataaattta acgaaagaat agaaagggcc ttaacacgag ggattcaactg catcttacaa	540
acccaggta aacaaggaga taaactaacc atctggccg cacagtagca tcagaaaaca	600
atggAACCTG ctcaagccag actgtttgaa ccggtagcgt taggcacagc ggaatcgccg	660
ggcattctcc gcttttaat gcgttgcac catcctactc ccggaaataaa aaatgcaatc	720
aaccacgctg tagaatgggt ttcctccat aaagaggtag gctatgatta cgttaaaacg	780
gaaaaaaaaacg gaaaactttt gcgggatttg gtttctcgc ccggctctac cgtatggca	840
agattttatg acatcaggac gaatcaaccc atcttgggt atcgcgataa tacgataaag	900
tattcgctga atgaaataag cgaggaacga caaaatggct actcttggta tggtaactgg	960
ccagaaaaga taattacaaa agaatatgaa aaatggctta agaaggtaaa tgaataa	1017

<210> 114

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(18)

<221> DOMAIN

<222> (19)...(388)

<223> Catalytic domain

<400> 114

Met Lys Ile Phe Leu Thr Ile Leu Leu Ser Ala Leu Phe Ser Ile Ser			
1	5	10	15
Asn Ala Gln Val Leu Ser Asp Pro Val Ala Asp Arg Met Thr Ser Tyr			
20	25	30	
Gln Leu Lys Asn Gly Gly Trp Pro Lys His Leu Ala Asp Lys Ser Val			
35	40	45	
Val Asn Tyr Ser Lys Pro Leu Ser Pro Ala Leu Gln Lys Val Ile Asp			
50	55	60	

Gln Ser Thr Glu Lys Ser Ala Thr Ile Asp Asn Asn Ala Thr Thr Arg
 65 70 75 80
 Glu Ile Asn His Leu Leu Leu Ala Tyr Ser Lys Thr Asn Asn Asp Lys
 85 90 95
 Tyr Leu Gln Ala Ala Thr Lys Gly Val Glu Tyr Ile Leu Ser Ala Gln
 100 105 110
 Asn Asp Lys Gly Gly Trp Pro Gln Tyr Tyr Pro Asp Ser Ser Ser Tyr
 115 120 125
 Arg Gly Gln Ile Thr Tyr Asn Asp Gly Ala Met Ile Asn Val Leu Glu
 130 135 140
 Ile Leu Leu Ser Ile Ser Thr Lys Gln Glu Pro Tyr Ala Val Leu Thr
 145 150 155 160
 Asn Lys Phe Asn Glu Arg Ile Glu Arg Ala Leu Thr Arg Gly Ile His
 165 170 175
 Cys Ile Leu Gln Thr Gln Val Lys Gln Gly Asp Lys Leu Thr Ile Trp
 180 185 190
 Ala Ala Gln Tyr Asp Gln Lys Thr Met Glu Pro Ala Gln Ala Arg Leu
 195 200 205
 Phe Glu Pro Val Ala Leu Ala Thr Ala Glu Ser Ala Gly Ile Leu Arg
 210 215 220
 Phe Leu Met Arg Leu Asp His Pro Thr Pro Glu Ile Lys Asn Ala Ile
 225 230 235 240
 Asn His Ala Val Glu Trp Phe Ser Ser His Lys Glu Val Gly Tyr Asp
 245 250 255
 Tyr Val Lys Thr Glu Lys Asn Gly Lys Leu Leu Arg Asp Leu Val Ser
 260 265 270
 Ser Pro Ala Ser Thr Val Trp Ala Arg Phe Tyr Asp Ile Arg Thr Asn
 275 280 285
 Gln Pro Ile Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Ser Leu Asn
 290 295 300
 Glu Ile Ser Glu Glu Arg Gln Asn Gly Tyr Ser Trp Tyr Gly Asn Trp
 305 310 315 320
 Pro Glu Lys Ile Ile Thr Lys Glu Tyr Glu Lys Trp Leu Lys Lys Val
 325 330 335
 Asn Glu

<210> 115
 <211> 996
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 115
 gtggccaagg cgatccggcg tccgttgccg ccggcaccag ggcaggatc gcccgttaacg 60
 tggcgacga ttctccggca gccatcgccg tggtaacgcgt ccgcggacgc gaaggcggtt 120
 gccgaaaccg tgcgcgcgag ccagagagcc accggcggtc ggccgaagaa cacgattgg 180
 acggcgctcc agagcgacgc tgagcgccag ggcgtcgaa atgcccgcgc cgagaccgat 240
 tcgacgatcg acaatggcgc cacggtcacc gagcttcgtt ttctaccgg cgttatgtc 300
 gccacgcgcg acgagcttt acgggaggcc gtgcttcgcg gcctcgacta cctgctggcg 360
 tcgcagtaca gcaacggcg ctggccacaa tacttccgt tgccgaccga ttactcgccg 420
 gacatcacgt tcaacgacga cgcgttgacc ggcgtggcgc tgctgctgaa ggatgcccgc 480
 gacgggtcag caggttgcgatcgtcgac aaggcgagac gtgaccgcgc tgccgcggcc 540
 gtgacgcgcg ccatcgccgt gatcctccgc acgcagattc gggtaacgg tacgctgacc 600
 ggctggcgc acgactacga cgccgacgcg ctgacgcccgg cgccgcggcc ctcgtacgag 660
 catccgtcga ttgcgagccg cgagacggc gggatcgccg ggctgctgat gggctgtccg 720
 aatccgtcgc cagagatcgt ggctgcccgtt gacgcggctg ccgcattgtt gggtaaatcg 780

gaactgaagg	gtgtgccccga	ggcgacggcg	ccaggacttt	gggcgcgcctt	ctacgacatc	840
gctacgaatc	ggccgatcta	ttcgggcccgc	gacggcggtca	tcaagtacccg	gctcgacgag	900
atcgagctcg	agcggcgac	aggctacacgc	tgggttggcc	cgtacgcccgc	ggcatttctg	960
acgaccgaat	atccgaaaatg	gcggggcggca	cgatga			996

<210> 116
<211> 331
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(331)
<223> Catalytic domain

<400> 116
Met Ala Lys Ala Ile Gly Gly Pro Leu Pro Pro Ala Pro Gly Gln Gly
1 5 10 15
Ser Pro Val Thr Trp Ala Thr Ile Leu Arg Gln Pro Ser Pro Trp Tyr
20 25 30
Ala Ser Ala Asp Ala Lys Ala Val Ala Glu Thr Val Arg Ala Ser Gln
35 40 45
Arg Ala Thr Gly Gly Trp Pro Lys Asn Thr Asp Trp Thr Ala Leu Gln
50 55 60
Ser Asp Ala Glu Arg Gln Ala Leu Arg Asn Ala Arg Ala Glu Thr Asp
65 70 75 80
Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Glu Leu Arg Phe Leu Thr
85 90 95
Arg Val Tyr Val Ala Thr Arg Asp Glu Leu Leu Arg Glu Ala Val Leu
100 105 110
Arg Gly Leu Asp Tyr Leu Leu Ala Ser Gln Tyr Ser Asn Gly Gly Trp
115 120 125
Pro Gln Tyr Phe Pro Leu Arg Thr Asp Tyr Ser Arg Asp Ile Thr Phe
130 135 140
Asn Asp Asp Ala Met Thr Gly Val Val Leu Leu Lys Asp Ala Ala
145 150 155 160
Asp Gly Ser Ala Gly Phe Glu Phe Val Asp Lys Ala Arg Arg Asp Arg
165 170 175
Ala Ala Ala Ala Val Thr Arg Ala Ile Ala Val Ile Leu Arg Thr Gln
180 185 190
Ile Arg Val Asn Gly Thr Leu Thr Gly Trp Cys Gln Gln Tyr Asp Ala
195 200 205
Asp Ala Leu Thr Pro Ala Arg Gly Arg Ser Tyr Glu His Pro Ser Ile
210 215 220
Ala Ser Arg Glu Thr Val Gly Ile Ala Arg Leu Leu Met Gly Val Pro
225 230 235 240
Asn Pro Ser Pro Glu Ile Val Ala Ala Val Asp Ala Ala Ala Trp
245 250 255
Leu Gly Lys Ser Glu Leu Lys Gly Val Pro Glu Ala Thr Ala Pro Gly
260 265 270
Leu Trp Ala Arg Phe Tyr Asp Ile Ala Thr Asn Arg Pro Ile Tyr Ser
275 280 285
Gly Arg Asp Gly Val Ile Lys Tyr Arg Leu Asp Glu Ile Glu Leu Glu
290 295 300
Arg Arg Thr Gly Tyr Ser Trp Val Gly Pro Tyr Ala Ala Ala Phe Leu
305 310 315 320
Thr Thr Glu Tyr Pro Lys Trp Arg Ala Ala Arg

325

330

<210> 117
<211> 1725
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 117

atgaagaatt	ttgggtttgg	taactacaag	ttttttgtag	cgccaatgtc	tgtcgctct	60
tttcgtatg	cgccaagcta	tacacccccc	tcaacacgcg	tttcgaaaat	caacagctat	120
cgaggctatt	cggagctgac	ttcagctgca	tccggcatgg	atatcgacca	gtacacacctac	180
aacatgacca	cttggcaaatt	cgcacacggc	ggttttaca	aagccatggc	cgacaaggat	240
aaaagcgcgt	atggcgccgg	tcaaaaatcc	aatggcaag	ctaaaggccg	tggcgacctc	300
ggcactatag	acaacaacgc	caccatccag	gaaatgcgtt	tgctcgccgt	gcgttacaaa	360
gaaacgacga	acaacaatta	caaattccgc	tttaagacaa	gttcaacaa	ggcggtcaat	420
tttctttga	ccatgcagcg	ctccaaaggc	ggactccac	aagtttggcc	caaacgcggc	480
aactattctg	accaaatcac	gctaaatgac	aacgccatga	tccgcgcac	ggtcacgatg	540
atggatatcg	ccaacaagac	gagtccattt	gattcgata	tcatgcacga	cgccacccgc	600
agcaaaatga	aatcggtct	cgacaaagcg	gtcgattact	tgctcaaggc	gcaaatcgtg	660
aacgacggaa	aggtcacgg	atggtgcc	cagcacgaca	ccaacagcc	cgccccgt	720
ggcgacacgag	cctacgaact	cccgagcaaa	tccggcaacg	aatccatggg	cgttgtgtgg	780
tttttgcata	actggccaga	ccaaaacgaa	gcaatccaga	aggcggtcaa	aggcgcaatc	840
gcttggtaca	aaaagaataa	actaaaagac	aaggcgaaa	gcaagaccgc	aggcggtgtg	900
gacaaggcgg	gttcatcgct	gtgggtccgc	ttttacgaag	tcaacaacga	caactacttt	960
ttctgcgacc	gcgtatggc	tagcaccaag	acgcaggact	tcatgaaaat	cagcgaagaa	1020
cgtcgcaagg	gctaccatgt	ggcaggcgat	tacggctctg	caattctagg	caccggaaaat	1080
gcataccctt	aagcactcgc	caagatggac	gacaactatg	ttccacctcc	gccagcacca	1140
gctatgtgcg	gaaacgacac	ttgcaaaacg	tacatcgatg	gcgttgactt	tattgacatt	1200
caaggcgtca	aggaaacaac	caacacggg	ttcggtggcg	aaggttacgc	caacgttgac	1260
aactccaccc	gaagctatgt	gacctacggc	gtcaccgc	tcaaggaagg	caaatacact	1320
ttgttcatca	gctttgcaaa	cgcggtgg	tccgcacgc	gttacagcg	ttctgcagga	1380
gacaagacgt	tacttgcaga	cgcgacat	aatctacag	ccgcatggac	cacttggaaa	1440
atgcaatcca	tcgaaatcga	attgccaatg	ggctatagcg	aactcaagtt	cacaagcctt	1500
tcgaaagacg	gtatggcgaa	catcgattac	atcggtgg	tgaacgatga	tttggaaagtt	1560
ggcgaagttg	aagtaccacg	ctcatccatt	gaagcaatac	gcccacatcc	caaagcccg	1620
caggacaacc	gctacttgt	ggactttggc	ggcaacaata	atagcgcagg	ggcttacttt	1680
aagcgtggca	tcaacacgtt	ccgcgtgaat	gggaagatga	ggtaa		1725

<210> 118
<211> 574
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(24)

<221> DOMAIN
<222> (25)...(574)
<223> Catalytic domain

<400> 118
Met Lys Asn Phe Gly Phe Gly Asn Tyr Lys Phe Phe Val Ala Ala Met
1 5 10 15

Ser Val Ala Ser Phe Ser Tyr Ala Ala Ser Tyr Thr Pro Pro Ser Thr
 20 25 30
 Ala Val Ser Lys Ile Asn Ser Tyr Arg Gly Tyr Ser Glu Leu Thr Ser
 35 40 45
 Ala Ala Ser Gly Met Asp Ile Asp Gln Tyr Thr Tyr Asn Met Thr Thr
 50 55 60
 Trp Gln Ile Ala Asn Gly Gly Phe Tyr Lys Ala Met Ala Asp Lys Tyr
 65 70 75 80
 Lys Ser Ala Tyr Gly Gly Gln Lys Ser Glu Trp Gln Ala Lys Gly
 85 90 95
 Gly Gly Asp Leu Gly Thr Ile Asp Asn Asn Ala Thr Ile Gln Glu Met
 100 105 110
 Arg Leu Leu Ala Val Arg Tyr Lys Glu Thr Thr Asn Asn Tyr Lys
 115 120 125
 Ser Ala Phe Lys Thr Ser Phe Asn Lys Ala Val Asn Phe Leu Leu Thr
 130 135 140
 Met Gln Arg Ser Lys Gly Gly Leu Pro Gln Val Trp Pro Lys Arg Gly
 145 150 155 160
 Asn Tyr Ser Asp Gln Ile Thr Leu Asn Asp Asn Ala Met Ile Arg Ala
 165 170 175
 Met Val Thr Met Met Asp Ile Ala Asn Lys Thr Ser Pro Phe Asp Ser
 180 185 190
 Asp Ile Ile Asp Asp Ala Thr Arg Ser Lys Met Lys Ser Ala Leu Asp
 195 200 205
 Lys Ala Val Asp Tyr Leu Leu Lys Ala Gln Ile Val Asn Asp Gly Lys
 210 215 220
 Val Thr Val Trp Cys Ala Gln His Asp Thr Asn Ser Leu Ala Pro Val
 225 230 235 240
 Gly Ala Arg Ala Tyr Glu Leu Pro Ser Lys Ser Gly Asn Glu Ser Met
 245 250 255
 Gly Val Val Trp Phe Leu Met Asn Trp Pro Asp Gln Asn Glu Ala Ile
 260 265 270
 Gln Lys Ala Val Lys Gly Ala Ile Ala Trp Tyr Lys Lys Asn Lys Leu
 275 280 285
 Lys Asp Lys Ala Phe Ser Lys Thr Ala Gly Val Val Asp Lys Ala Gly
 290 295 300
 Ser Ser Leu Trp Phe Arg Phe Tyr Glu Val Asn Asn Asp Asn Tyr Phe
 305 310 315 320
 Phe Cys Asp Arg Asp Gly Ala Ser Thr Lys Thr Gln Asp Phe Met Lys
 325 330 335
 Ile Ser Glu Glu Arg Arg Lys Gly Tyr Gln Trp Ala Gly Asp Tyr Gly
 340 345 350
 Ser Ala Ile Leu Gly Thr Glu Asn Ala Tyr Leu Glu Ala Leu Ala Lys
 355 360 365
 Met Asp Asp Asn Tyr Val Pro Pro Pro Pro Ala Pro Ala Met Cys Gly
 370 375 380
 Asn Asp Thr Cys Lys Thr Tyr Ile Asp Gly Val Asp Phe Ile Asp Ile
 385 390 395 400
 Gln Gly Val Lys Glu Thr Thr Asn Thr Gly Phe Val Gly Glu Gly Tyr
 405 410 415
 Ala Asn Val Asp Asn Ser Thr Gly Ser Tyr Val Thr Tyr Gly Val Thr
 420 425 430
 Ala Phe Lys Glu Gly Lys Tyr Thr Leu Phe Ile Ser Phe Ala Asn Gly
 435 440 445
 Gly Gly Ser Ala Arg Gly Tyr Ser Val Ser Ala Gly Asp Lys Thr Leu
 450 455 460
 Leu Ala Asp Gly Ser Met Glu Ser Thr Ala Ala Trp Thr Thr Trp Lys
 465 470 475 480
 Met Gln Ser Ile Glu Ile Glu Leu Pro Met Gly Tyr Ser Glu Leu Lys

485	490	495													
Phe	Thr	Ser	Leu	Ser	Lys	Asp	Gly	Met	Ala	Asn	Ile	Asp	Tyr	Ile	Gly
500														510	
Trp	Met	Asn	Asp	Asp	Leu	Lys	Val	Gly	Glu	Val	Glu	Val	Pro	Arg	Ser
515														525	
Ser	Ile	Glu	Ala	Ile	Arg	Ala	Ile	Arg	Lys	Ala	Gln	Gln	Asp	Asn	Arg
530														540	
Tyr	Phe	Val	Asp	Phe	Gly	Gly	Asn	Asn	Asn	Ser	Ala	Gly	Ala	Tyr	Phe
545														555	560
Lys	Arg	Gly	Ile	Asn	Thr	Phe	Arg	Val	Asn	Gly	Lys	Met	Arg		
														565	570

<210> 119

<211> 1848

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 119

gtgtcatggc	aggaatccgg	tgcggctatc	accaacgcct	ggaatgcaac	gctcagtggc	60
tcaaaccctt	acacagccgt	atccgctggt	tggaaatggca	cacttgc(ccc	caatgcac	120
gccacttttg	gttccaggc	aaacggttct	gcccgtgcac	ctaaagtgaa	tggcagctt	180
tgcggcacca	acacttcatc	aacacccggca	tccagcagt	ttgcccagctc	ggttaaatca	240
agcgcgcccc	tatcgccag	cagcagatca	tccagttcaa	tcgctatcac	tagcagctc	300
ttagcgagaa	gttctattgc	ctccagcagc	tcactagtt	gtagctccag	agcgagcagt	360
agtgcgccaa	gcgttttctc	ttttacgatc	caggaagagc	aagcgggctt	ctgtcgtgtt	420
gatggcattt	cgacagaaaag	caccaacacc	ggttttaccg	gcaatggcta	caccaatgcg	480
aacaacgcgc	aaggcgcagc	gattgaatgg	gcagtcagcg	cacctagcag	tggccgttat	540
acagtagcct	tccgcttcgc	caatggcggc	acagcagcgc	gcaacggctc	gttgttaatc	600
aatggcggta	gcaatggtaa	ttacactgtt	gagttacccc	tgaccggcgc	atggcaacc	660
tggcaaattt	ccagcgttga	aattgattt	gtgcaaggca	ataatattt	aaaactctcg	720
gcgttaaccg	ctgacggttt	ggccaatattc	gactcattaa	aaatagacgg	cgcgc当地	780
aaagcaggta	cttgcagcac	tacatcaagc	agcagcgtt	ccagcagctc	gtcgtccgtt	840
aatatccagcg	caagtttttc	ttcgagttca	tccaccgctg	caaaaataact	gacattagac	900
ggtaaccgg	ccgcccagct	gttcaacaaa	tccaggacca	agtggatag	cagccgc当地	960
gatatttgtt	tgtcttacca	gcaatccaac	ggcggttggc	caaaaaaccc	ggattacaac	1020
tcagtgcgc	caggcaatgg	cgggagcgcac	agcggcacca	tgcacaatgg	tgcaaccatt	1080
accggaaatgg	tttacctcgc	tggaaatttat	aaaaacggcg	gcaacaccaa	atatcgcat	1140
gcagtgcgc	gagcagcaaa	cttttagtg	agctcgcaat	acagcacagg	cgccttgc当地	1200
caattttatc	cggtgaaagg	cgctatgcgc	gatcatgcga	cctttaacga	taacggcat	1260
gcgtacgcgt	tgacggattt	ggatttcgc	gtaaacaaac	gcgcaccgtt	tgataacgc	1320
attttctctg	attctgatcg	ggcggaaattt	aaaacgcgt	ttgccaaagg	tgtggattac	1380
attttaaaag	cgcagtggaa	acaaaatgg	aaactcact	catggtgtc	acaacacgg	1440
gctacggatt	accaaccgaa	aaaagcgcgc	gcttatgaat	tggaaatcatt	gagtggtagc	1500
gagtcggatc	gcatttcgc	cttcttgcgt	acccaaccac	aaaccgcgc	aatcgaagcg	1560
gcgggtcaagg	cgggtgtcaa	ctgggtcgcc	agtccaaata	cttatttggc	taactacact	1620
tacgattcat	aaaaacgcgc	taccaacccg	attgtgtata	aatccggaag	cagaatgtgg	1680
tatcgcttct	atgacctgaa	caccaaccgt	ggtttcttta	gtgatcgca	tggcagcaaa	1740
ttctatgata	tcacccaaat	gtcagaagag	cgtcgaccg	ttatagctg	gggtggctt	1800
	tacggtaat	cttattttc	cttcgcgc当地	aaagtgggtt	atctgtaa	1848

<210> 120

<211> 615

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> BINDING

<222> (1)...(61)

<223> Carbohydrate binding module

<221> BINDING

<222> (134)...(257)

<223> Carbohydrate binding module

<221> DOMAIN

<222> (258)...(615)

<223> Catalytic domain

<400> 120

Met	Ser	Trp	Gln	Glu	Ser	Gly	Ala	Ala	Ile	Thr	Asn	Ala	Trp	Asn	Ala
1			5				10					15			
Thr	Leu	Ser	Gly	Ser	Asn	Pro	Tyr	Thr	Ala	Val	Ser	Ala	Gly	Trp	Asn
			20				25					30			
Gly	Thr	Leu	Ala	Pro	Asn	Ala	Ser	Ala	Thr	Phe	Gly	Phe	Gln	Ala	Asn
			35				40					45			
Gly	Ser	Ala	Gly	Ala	Pro	Lys	Val	Asn	Gly	Ser	Leu	Cys	Gly	Thr	Asn
			50			55					60				
Thr	Ser	Ser	Thr	Pro	Ala	Ser	Ser	Ser	Val	Ala	Ser	Ser	Val	Lys	Ser
			65			70					75			80	
Ser	Ala	Pro	Val	Ser	Ser	Ser	Arg	Ser	Ser	Ser	Ile	Ala	Ile		
			85				90					95			
Thr	Ser	Ser	Ser	Leu	Ala	Arg	Ser	Ile	Ala	Ser	Ser	Ser	Leu		
			100			105					110				
Val	Ser	Ser	Arg	Ala	Ser	Ser	Ala	Pro	Ser	Val	Phe	Ser	Phe		
			115			120					125				
Thr	Ile	Gln	Glu	Glu	Gln	Ala	Gly	Phe	Cys	Arg	Val	Asp	Gly	Ile	Ala
			130			135					140				
Thr	Glu	Ser	Thr	Asn	Thr	Gly	Phe	Thr	Gly	Asn	Gly	Tyr	Thr	Asn	Ala
			145			150					155			160	
Asn	Asn	Ala	Gln	Gly	Ala	Ala	Ile	Glu	Trp	Ala	Val	Ser	Ala	Pro	Ser
						165					170			175	
Ser	Gly	Arg	Tyr	Thr	Val	Ala	Phe	Arg	Phe	Ala	Asn	Gly	Gly	Thr	Ala
			180			185						190			
Ala	Arg	Asn	Gly	Ser	Leu	Leu	Ile	Asn	Gly	Gly	Ser	Asn	Gly	Asn	Tyr
			195			200					205				
Thr	Val	Glu	Leu	Pro	Leu	Thr	Gly	Ala	Trp	Ala	Thr	Trp	Gln	Ile	Ala
			210			215					220				
Ser	Val	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Ile	Leu	Lys	Leu	Ser
			225			230					235			240	
Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys	Ile	Asp
						245					250			255	
Gly	Ala	Gln	Thr	Lys	Ala	Gly	Thr	Cys	Ser	Thr	Thr	Ser	Ser	Ser	Ser
						260					265			270	
Val	Ala	Ser	Ser	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Ser
			275			280					285				
Ser	Ser	Ser	Thr	Ala	Ala	Lys	Ile	Leu	Thr	Leu	Asp	Gly	Asn	Pro	Ala
			290			295					300				
Ala	Ser	Trp	Phe	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Ser	Ser	Arg	Ala
			305			310					315			320	
Asp	Ile	Val	Leu	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys	Asn
						325					330			335	
Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Asp	Ser	Gly
						340					345			350	

Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu
 355 360 365
 Ile Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg
 370 375 380
 Ala Ala Asn Phe Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro
 385 390 395 400
 Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn
 405 410 415
 Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn
 420 425 430
 Lys Arg Ala Pro Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala
 435 440 445
 Lys Phe Lys Thr Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala
 450 455 460
 Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly
 465 470 475 480
 Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser
 485 490 495
 Leu Ser Gly Ser Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln
 500 505 510
 Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp
 515 520 525
 Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser
 530 535 540
 Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met Trp
 545 550 555 560
 Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg
 565 570 575
 Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg
 580 585 590
 Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser Phe
 595 600 605
 Ala Gln Lys Val Gly Tyr Leu
 610 615

<210> 121

<211> 1047

<212> DNA

<213> Bacteria

<400> 121

atgatgagat caagcatcgt caagctagtt	gctttcagtg ttgtggttat	gttatggctc	60		
ggtgtatcct ttcaaacggc	agaagcgaat acgccaaatt	tcaacttaca	aggcttgcc	120	
acgttaaatg gggacaacaac	tgggtgtgca	ggtgagatg	tagtgcgg	180	
aatgaattaa taaacgttt	gaagtccaaa	aaccctaatac	tcgtacaggg	240	
aacggtaga taacacccat	taatacgtct	gatagtaaga	tcgatattaa	ggatgtttcc	300
aatgtatcga ttttaggggt	tgtacaaat	ggacgattaa	atgggatcg	tattaaagta	360
tggcgagcga ataataatcat	cattcgcaac	ttgacgatcc	atgaagtcca	tacaggttat	420
aaagatgcga ttagcattga	aggccctct	cgaaacattt	ggattgacca	taacgagtt	480
tatgccagct tgaacgttca	taaagaccac	tatgacggct	tgttgcacgt	aaagcgcgt	540
gcttacaata ttaccttctc	ttgaaattat	gtccatgtg	gctggaaagc	gatgctcatg	600
gggaactctg atagtataaa	ctacgaccga	aacataacat	tccaccataa	ctacttcaaa	660
aacttaaact ctgcgttacc	tgctgtaccgt	tttggaaagg	cgcacttgtt	tagcaattac	720
tttgagaaca ttttagaaac	aggcattaat	tcacggatgg	gagcggaaat	gctcggtgaa	780
cataacgttt ttgagaatgc	caccaacccg	ttaggattct	ggcatagca	tgcacaggt	840
tatttggatg ttgccaataa	ccgctataatc	aatagcacgg	gtacatgcc	gaccacttcc	900
acgaccaatt atcgacccctc	ttatccctat	acggtcacac	cagttggtga	tgtgaaatcg	960
gttgcacac gttatgcggg	agttggtgtc	atccagccgt	atgcaagaaa	gccccatccgag	1020
cgattgctct ggtggcttt	tgcataa				1047

<210> 122
<211> 348
<212> PRT
<213> Bacteria

<220>

<221> SIGNAL
<222> (1)...(29)

<221> DOMAIN
<222> (30)...(348)
<223> Catalytic domain

<400> 122
Met Met Arg Ser Ser Ile Val Lys Leu Val Ala Phe Ser Val Val Val
1 5 10 15
Met Leu Trp Leu Gly Val Ser Phe Gln Thr Ala Glu Ala Asn Thr Pro
20 25 30
Asn Phe Asn Leu Gln Gly Phe Ala Thr Leu Asn Gly Gly Thr Thr Gly
35 40 45
Gly Ala Gly Gly Asp Val Val Thr Val Arg Thr Gly Asn Glu Leu Ile
50 55 60
Asn Ala Leu Lys Ser Lys Asn Pro Asn Arg Pro Leu Thr Ile Tyr Val
65 70 75 80
Asn Gly Thr Ile Thr Pro Ser Asn Thr Ser Asp Ser Lys Ile Asp Ile
85 90 95
Lys Asp Val Ser Asn Val Ser Ile Leu Gly Val Gly Thr Asn Gly Arg
100 105 110
Leu Asn Gly Ile Gly Ile Lys Val Trp Arg Ala Asn Asn Ile Ile Ile
115 120 125
Arg Asn Leu Thr Ile His Glu Val His Thr Gly Asp Lys Asp Ala Ile
130 135 140
Ser Ile Glu Gly Pro Ser Arg Asn Ile Trp Ile Asp His Asn Glu Leu
145 150 155 160
Tyr Ala Ser Leu Asn Val His Lys Asp His Tyr Asp Gly Leu Phe Asp
165 170 175
Val Lys Arg Asp Ala Tyr Asn Ile Thr Phe Ser Trp Asn Tyr Val His
180 185 190
Asp Gly Trp Lys Ala Met Leu Met Gly Asn Ser Asp Ser Asp Asn Tyr
195 200 205
Asp Arg Asn Ile Thr Phe His His Asn Tyr Phe Lys Asn Leu Asn Ser
210 215 220
Arg Val Pro Ala Tyr Arg Phe Gly Lys Ala His Leu Phe Ser Asn Tyr
225 230 235 240
Phe Glu Asn Ile Leu Glu Thr Gly Ile Asn Ser Arg Met Gly Ala Glu
245 250 255
Met Leu Val Glu His Asn Val Phe Glu Asn Ala Thr Asn Pro Leu Gly
260 265 270
Phe Trp His Ser Ser Arg Thr Gly Tyr Trp Asn Val Ala Asn Asn Arg
275 280 285
Tyr Ile Asn Ser Thr Gly Ser Met Pro Thr Thr Ser Thr Thr Asn Tyr
290 295 300
Arg Pro Pro Tyr Pro Tyr Thr Val Thr Pro Val Gly Asp Val Lys Ser
305 310 315 320
Val Val Thr Arg Tyr Ala Gly Val Gly Val Ile Gln Pro Tyr Ala Arg
325 330 335
Lys Pro Ser Glu Arg Leu Leu Trp Trp Leu Phe Ala

340

345

<210> 123
 <211> 1830
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 123	60
ttgagtctac tttagttaat gacccttttgcctgtatgg caagtaacaa cgtagctccc	120
tggggctggg ccacctgctc cgatgagtca gcgcacagttt atactctgaa cggaggttgc	180
tttctgtatc catcttcgt tactctgaaa gctcttggca atgaacaaac agatgacaaa	240
caaatacaac aggctatcgc tcagaaagac atcattatct tagatggttc caatggcgat	300
ttcatcctta atgaatacat caagatttcg accaaaaaca aaaccatcat tggtatcaac	360
aaccccccc tggatcacaa gttctaccta accgctgatg atattacgtt ccttaaagca	420
caaggactgg agggactgag tagtacaaat caacatacag gaactctgccc tggatggcaca	480
acagtgcacct gtgacgagcg tggcttttc accaagaaag ccatcatgga actccaatat	540
cagaaaaacag gatcctatac cctacccaaat aaatcaggtt tcttttattt agatggcgct	600
tctgagaata tcatcatccg aaatatttcg ctgataggc caggagccgt agatataagac	660
ggagctgacc tgattacaa tcagggtaag cacgtctgga ttgaccattt caccgttgc	720
gactctcaag atgggtccct ggacagcaag gtatgcact gggccaccta tacctataac	780
cacttctact atacagaccg cagttactca catgcttaca cttgcgggtt cggatgggtc	840
agcaatcatg aaatgggtat tcacatgacc tttgcatgtt atatctgggg agcaaaatgt	900
atgcgtcgct tgccgcaagc agatgactgt ttcatacacc ttgtgaacaa ctatcacaac	960
tgtcctggca atagtgtcggtatgaccatt aacagttaca gcaaaagcatt gtttgagggt	1020
aactatgctg ctgcagggtt caacaagcca ttagatggca gtggggccaa cgcgtatgtt	1080
acagctaagg ataatagttt tgccaaactca caagccgtt ctgttgc tgcgtccatac	1140
gactatacca agattgcgc cccgcacgtt ccagctacgc tgactggaaac agagggtgca	1200
ggcccccacat taggcaacga tgcacacatac attctgtcta ctattccaaat tgcgaccga	1260
caagaaggcg aatcttcaact ctactatttc attgtatggcc tgggtggaaac taataatgaa	1320
ggcttattcca ttatagagtt taatgtatggc gcaacattgc tgctgaacaa taaagagaaa	1380
gcatggctta atggtagtgc aattcaactt ggtgacgata attatacggat tattaaactt	1440
tctaatggag cagaaaaacat cttcacagca cctactggca aaaaagtaag tggattacc	1500
ttctattttt atatcaatataaaatcaactt tcacccaaata tccagaatata	1560
ggtttccgca cctgttctg gcagaaagtt gccaacctca cttattctgc gactttctgat	1620
gacgtacaaa tcttgaatc tcgtatcca cagaatactg acgtggcattt attccatttc	1680
actccaaacaa atgttgcgtt tttcaaaaat tcaggtgaac agctttgtttt cttatgaaa	1740
gtcacctata gtgatgaaag cacaggttac tctgctatcc agaaaaaaat gcctatcgat	1800
ggcgttacccataataacccatca aggtatccgt atagataatc ccaccaaggaa aatctatatt	1830
cagaacggaa agaaaatcat tatcaaataaa	

<210> 124
 <211> 609
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(390)
 <223> Catalytic domain

<400> 124

Leu Ser Leu Leu Ser Val Met Thr Leu Leu Pro Val Met Ala Ser Asn
 1 5 10 15
 Asn Val Ala Pro Trp Gly Trp Ala Thr Cys Ser Asp Glu Ser Ala Thr
 20 25 30
 Ala Tyr Thr Leu Asn Gly Gly Cys Phe Ser Asp Ala Ser Ser Val Thr
 35 40 45
 Leu Lys Ala Leu Gly Asn Glu Gln Thr Asp Asp Lys Gln Ile Lys Gln
 50 55 60
 Ala Ile Ala Gln Lys Asp Ile Ile Ile Leu Asp Gly Ser Asn Gly Asp
 65 70 75 80
 Phe Ile Leu Asn Glu Tyr Ile Lys Ile Ser Thr Lys Asn Lys Thr Ile
 85 90 95
 Ile Gly Ile Asn Asn Ala Arg Leu Cys Thr Lys Phe Tyr Leu Thr Ala
 100 105 110
 Asp Asp Ile Thr Tyr Leu Lys Ala Gln Gly Leu Glu Gly Leu Ser Ser
 115 120 125
 Thr Asn Gln His Thr Gly Thr Leu Pro Asp Gly Thr Thr Val Thr Cys
 130 135 140
 Asp Glu Arg Ala Phe Phe Thr Lys Lys Ala Ile Met Glu Leu Gln Tyr
 145 150 155 160
 Gln Lys Thr Gly Ser Tyr Thr Leu Pro Asn Lys Ser Gly Ile Phe Tyr
 165 170 175
 Leu Asp Ala Ala Ser Glu Asn Ile Ile Arg Asn Ile Ser Leu Ile
 180 185 190
 Gly Pro Gly Ala Val Asp Ile Asp Gly Ala Asp Leu Ile Thr Asn Gln
 195 200 205
 Gly Lys His Val Trp Ile Asp His Cys Thr Phe Val Asp Ser Gln Asp
 210 215 220
 Gly Ala Leu Asp Ser Lys Val Cys Asp Trp Ala Thr Tyr Thr Tyr Asn
 225 230 235 240
 His Phe Tyr Tyr Thr Asp Arg Ser Tyr Ser His Ala Tyr Thr Cys Gly
 245 250 255
 Cys Gly Trp Val Ser Asn His Glu Met Val Ile His Met Thr Phe Ala
 260 265 270
 Cys Asn Ile Trp Gly Ala Lys Cys Met Arg Arg Leu Pro Gln Ala Asp
 275 280 285
 Asp Cys Phe Ile His Leu Val Asn Asn Tyr His Asn Cys Pro Gly Asn
 290 295 300
 Ser Val Gly Met Thr Ile Asn Ser Tyr Ser Lys Ala Leu Val Glu Gly
 305 310 315 320
 Asn Tyr Ala Ala Ala Gly Val Asn Lys Pro Leu Asp Gly Ser Gly Ala
 325 330 335
 Asn Arg Asn Val Thr Ala Lys Asp Asn Ser Phe Ala Asn Ser Gln Ala
 340 345 350
 Gly Ser Val Val Ser Val Pro Tyr Asp Tyr Thr Lys Ile Ala Ala Ala
 355 360 365
 Asp Val Pro Ala Thr Leu Thr Gly Thr Glu Gly Ala Gly Ala Thr Leu
 370 375 380
 Gly Asn Asp Ala Thr Tyr Ile Leu Ser Thr Ile Pro Thr Val Asp Arg
 385 390 395 400
 Gln Glu Gly Glu Ser Ser Leu Tyr Tyr Phe Ile Asp Gly Leu Val Gly
 405 410 415
 Thr Asn Ser Glu Gly Tyr Ser Ile Ile Glu Phe Asn Asp Gly Ala Thr
 420 425 430
 Leu Leu Leu Asn Asn Lys Glu Lys Ala Trp Ser Asn Gly Ser Ala Ile
 435 440 445
 Gln Leu Gly Asp Asp Asn Tyr Thr Ser Ile Lys Leu Ser Asn Gly Ala
 450 455 460
 Glu Asn Ile Phe Thr Ala Pro Thr Gly Lys Lys Val Ser Gly Ile Thr

465	470	475	480												
Phe	Tyr	Ser	Tyr	Ile	Asn	Ile	Lys	Glu	Glu	Lys	Leu	Asp	Phe	Thr	Lys
485								490						495	
Tyr	Pro	Glu	Tyr	Gly	Phe	Arg	Thr	Cys	Phe	Trp	Gln	Lys	Val	Ala	Asn
500								505						510	
Leu	Thr	Tyr	Ser	Ala	Thr	Ser	Asp	Asp	Val	Gln	Ile	Leu	Lys	Ser	Arg
515							520						525		
Asp	Pro	Gln	Asn	Thr	Asp	Val	Ala	Ser	Phe	His	Phe	Thr	Pro	Thr	Asn
530							535				540				
Val	Val	Ser	Phe	Lys	Asn	Ser	Gly	Glu	Gln	Leu	Cys	Phe	Leu	Met	Lys
545							550				555			560	
Val	Thr	Tyr	Ser	Asp	Glu	Ser	Thr	Gly	Ile	Ser	Ala	Ile	Gln	Lys	Lys
565							570						575		
Met	Pro	Ile	Asp	Gly	Val	Thr	Tyr	Asn	Leu	Gln	Gly	Ile	Arg	Ile	Asp
580							585						590		
Asn	Pro	Thr	Lys	Gly	Ile	Tyr	Ile	Gln	Asn	Gly	Lys	Lys	Ile	Ile	Ile
595							600						605		
Lys															

<210> 125

<211> 1170

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 125

atgaggtcta	aatatcatcg	cgccataaaat	aattatagtg	ttattattct	cgatggctcg	60
aatggcgatt	tcactattag	tgctacaatg	agttttagta	gcaaatcaaa	caaaaccata	120
gttgggttaa	ataatgctcg	cctatgcacc	aagtcttatac	taaccgatga	aataaagact	180
gcgcgtcgatg	ctgctaattgt	aaaatcagca	agttcaacca	gtggaggtgg	tacactctca	240
aatgggaaat	cagtgtcaga	acaacgtgaa	taccttactc	gtcaaacaat	tatcgatcta	300
actggcgatg	cttcggaaatc	gtgtcagaaa	gcgggcatct	ttagcttcag	tagttgtacc	360
aatatcatca	tgcgaaacct	cgtttgggt	ggccctggcc	catgcgatgt	aggtggcaac	420
gatttgctt	cgctcactgg	ttctaagcat	ttttgggtcg	atcactgtga	gttaaccgat	480
ggtatagatg	gcaatttcga	tattaccaag	agtagcgtt	tcaatactgt	tacttgggt	540
atattcaatt	ataccgatcg	tgcatacgcac	cacatgaact	ccaatcttat	tggtagctcc	600
gatagcgaag	atgctgccta	tttgaacact	actatggcat	gcaatatttgc	gggctacaag	660
tgcaatcagc	gaatgc当地	ggctcggtgc	ggtatattc	accttgc当地	caactttac	720
gattgc当地	gcaatagtgt	ggctgttaac	cctcgtaaaa	attctgagtt	cttagtc当地	780
aactgctact	ttgccacggg	tgtgaagccaa	ttctcgac	gtgggtgc当地	gggatacaac	840
tttattgatt	gctatacaga	agattcatac	actttcagc	agagtggtac	agtgtctgt	900
ccatacgaaa	actctaagtt	ttagtgc当地	ttagtacccg	agcaactcaa	taaatatgct	960
ggcgcaacgc	ttacttctcc	gcttgc当地	ggtc当地	agggtgttgc当地	tactcctatt	1020
agtgtctgt	ctgttgatag	cgatgtgt	ttgggtc当地	actattcgt	gactggtaat	1080
cggtttaaca	cgctcaatag	aggcatcaat	atcgtagaa	ctatattacgc	caacggcaaa	1140
gtaaccacac	aaaaggtttt	ggtgaaatag				1170

<210> 126

<211> 389

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> DOMAIN

<222> (24)...(325)
 <223> Catalytic domain

<400> 126
 Met Arg Ser Lys Ile Ile Ser Ala Ile Asn Asn Tyr Ser Val Ile Ile
 1 5 10 15
 Leu Asp Gly Ser Asn Gly Asp Phe Thr Ile Ser Ala Thr Met Ser Phe
 20 25 30
 Ser Ser Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
 35 40 45
 Cys Thr Lys Phe Tyr Leu Thr Asp Glu Ile Lys Thr Ala Leu Asp Ala
 50 55 60
 Ala Asn Val Lys Ser Ala Ser Ser Thr Ser Gly Gly Gly Thr Leu Ser
 65 70 75 80
 Asn Gly Lys Ser Val Ser Glu Gln Arg Glu Tyr Leu Thr Arg Gln Thr
 85 90 95
 Ile Ile Asp Leu Thr Gly Asp Ala Ser Glu Ser Cys Gln Lys Ala Gly
 100 105 110
 Ile Phe Ser Phe Ser Ser Cys Thr Asn Ile Ile Met Arg Asn Leu Val
 115 120 125
 Leu Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu Ser
 130 135 140
 Leu Thr Gly Ser Lys His Phe Trp Val Asp His Cys Glu Leu Thr Asp
 145 150 155 160
 Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn Thr
 165 170 175
 Val Thr Trp Cys Ile Phe Asn Tyr Thr Asp Arg Ala Tyr Asp His Met
 180 185 190
 Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asp Ala Ala Tyr Leu
 195 200 205
 Asn Thr Thr Met Ala Cys Asn Ile Trp Gly Tyr Lys Cys Asn Gln Arg
 210 215 220
 Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Phe Tyr
 225 230 235 240
 Asp Cys Ala Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser Glu
 245 250 255
 Phe Leu Val Glu Asn Cys Tyr Phe Ala Thr Gly Val Lys Pro Phe Ser
 260 265 270
 Gln Ser Gly Ala Leu Gly Tyr Asn Phe Ile Asp Cys Tyr Thr Glu Asp
 275 280 285
 Ser Tyr Thr Phe Gln Gln Ser Gly Thr Val Ser Val Pro Tyr Val Tyr
 290 295 300
 Ser Lys Phe Asp Val Gln Leu Val Pro Glu Gln Leu Asn Lys Tyr Ala
 305 310 315 320
 Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Glu Gly Val
 325 330 335
 Val Thr Pro Ile Ser Ala Val Ser Val Asp Ser Asp Val Val Leu Val
 340 345 350
 Glu Tyr Tyr Ser Leu Thr Gly Asn Arg Val Asn Thr Leu Asn Arg Gly
 355 360 365
 Ile Asn Ile Val Arg Thr Ile Tyr Ala Asn Gly Lys Val Thr Thr Gln
 370 375 380
 Lys Val Leu Val Lys
 385

<210> 127
 <211> 1449
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 127

atgcaatatg	gcaaattagt	acgcttgcg	gcactgacaa	cagcgctggc	attcagcgcc	60
ctggcacagg	caaataacct	ggcaattaca	ggccccggag	ccggggctga	tggttccagc	120
aaagccagtg	gcagtagcta	cggcgatgt	aaagacgccc	atctgcaaag	ctactggcaa	180
ccgcctgcta	ataacggcca	aagagtgtcg	gttaagtgg	gcagcgctat	cagcgtaat	240
caggtataac	tgcgtgaaca	gggcagtaat	gtaaccagct	gcccggctgg	aaataatgac	300
aacggcgcag	tattggcaac	cggcaccaggc	attggcagca	acagaacgg	taacttcagc	360
actgttaagca	cggaaaaact	caatctggaa	atactaactg	ccagcggtgc	cccgccgatt	420
gctgagttt	aagtttattt	aaataccaaat	ggccggcaacc	cgccaaatcc	tactgacc	480
gaaccaggcc	cggtaacttc	ttgcgcagcg	tctccacagg	gtatgcctc	gcttaacgg	540
ggcactaccg	gcccggcgtt	cagcaacgcg	gtcacggtaa	cggttaagcac	cggcgcctaa	600
atggtatcgg	cgctacaaaa	ccgcgatcta	aaccggccgc	tcactatccg	ggttaatggc	660
actatcacac	cgggtaattt	tggcggtgtc	agtaagttt	acattaaaga	tatggataat	720
gtcagcatta	ttggtgttag	caacaatgcg	ttgtttgacg	gtatcggtat	taaaatctgg	780
cgggccaata	acgttattat	ccgcaacac	acaatgcgtt	atgttaacac	cggcgataaaa	840
gacgctatta	ccattgaagg	cccgccgcgt	aatatctgg	ttgaccacaa	cgaaatctat	900
aacagcctga	atgtggtaa	agattttac	gacgagctt	taagcggtaa	aaaagacgta	960
gataacgtaa	ctatcttta	caactacctg	cacgacagct	ggaaaaccc	gctgtgggc	1020
agcagtgatt	ccgacaacta	caaccggcgt	attaccctt	accataacca	ctggcataaag	1080
gtaaattcac	gcctgccact	gttccgtttt	ggccaggggc	atatttacaa	taactattac	1140
aacgacattc	aggacaccgg	tattaacacg	cggatgggt	cggttaattcg	tattaaaaac	1200
aatgtgtttt	aaaacgcgaa	aaacccgata	gtgtcgttt	attccagcgg	ctacggttac	1260
tgggacaccc	gcggtaatag	cttagcaat	attacctggc	aggaataccc	cagcgcacggc	1320
attatcgccg	ggccaaatgt	acaacccaca	gcggtgctaa	acctgccccta	cagcttaac	1380
ctgttaccca	ccaaccagg	aaaagccac	gtactggcca	acgcggcgt	gaataaatgt	1440
atgttctaa						1449

<210> 128

<211> 482

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(24)

<221> DOMAIN

<222> (5)...(482)

<223> Catalytic domain

<400> 128

Met	Gln	Tyr	Gly	Lys	Leu	Val	Arg	Leu	Ser	Ala	Leu	Thr	Thr	Ala	Leu
1				5				10			15				
Ala	Phe	Ser	Ala	Leu	Ala	Gln	Ala	Asn	Asn	Leu	Ala	Ile	Thr	Gly	Pro
						20		25			30				
Gly	Ala	Gly	Ala	Asp	Gly	Ser	Ser	Lys	Ala	Ser	Gly	Ser	Ser	Tyr	Gly
				35		40		45							
Asp	Val	Lys	Asp	Ala	Asp	Leu	Gln	Ser	Tyr	Trp	Gln	Pro	Pro	Ala	Asn
						50		55		60					
Asn	Gly	Gln	Arg	Val	Ser	Val	Lys	Trp	Ser	Ser	Ala	Ile	Ser	Val	Asn
				65		70		75			80				
Gln	Val	Ile	Leu	Arg	Glu	Gln	Gly	Ser	Asn	Val	Thr	Ser	Trp	Arg	Leu
						85		90			95				

Val Asn Asn Asp Asn Gly Ala Val Leu Ala Thr Gly Thr Ser Ile Gly
 100 105 110
 Ser Asn Arg Thr Val Asn Phe Ser Thr Val Ser Thr Lys Lys Leu Asn
 115 120 125
 Leu Glu Ile Leu Thr Ala Ser Gly Ala Pro Arg Ile Ala Glu Phe Glu
 130 135 140
 Val Tyr Leu Asn Thr Asn Gly Gly Asn Pro Pro Asn Pro Thr Asp Pro
 145 150 155 160
 Glu Pro Gly Pro Val Thr Ser Cys Ala Ala Ser Pro Gln Gly Tyr Ala
 165 170 175
 Ser Leu Asn Gly Gly Thr Thr Gly Gly Ser Gly Ser Asn Ala Val Thr
 180 185 190
 Val Thr Val Ser Thr Gly Ala Gln Met Val Ser Ala Leu Gln Asn Arg
 195 200 205
 Asp Leu Asn Arg Pro Leu Thr Ile Arg Val Asn Gly Thr Ile Thr Pro
 210 215 220
 Gly Asn Ser Gly Gly Val Ser Lys Phe Asp Ile Lys Asp Met Asp Asn
 225 230 235 240
 Val Ser Ile Ile Gly Val Gly Asn Asn Ala Leu Phe Asp Gly Ile Gly
 245 250 255
 Ile Lys Ile Trp Arg Ala Asn Asn Val Ile Ile Arg Asn Leu Thr Met
 260 265 270
 Arg Tyr Val Asn Thr Gly Asp Lys Asp Ala Ile Thr Ile Glu Gly Pro
 275 280 285
 Ala Arg Asn Ile Trp Ile Asp His Asn Glu Ile Tyr Asn Ser Leu Asn
 290 295 300
 Val Gly Lys Asp Phe Tyr Asp Glu Leu Ile Ser Gly Lys Lys Asp Val
 305 310 315 320
 Asp Asn Val Thr Ile Ser Tyr Asn Tyr Leu His Asp Ser Trp Lys Thr
 325 330 335
 Ser Leu Trp Gly Ser Ser Asp Ser Asp Asn Tyr Asn Arg Arg Ile Thr
 340 345 350
 Phe His His Asn His Trp His Lys Val Asn Ser Arg Leu Pro Leu Phe
 355 360 365
 Arg Phe Gly Gln Gly His Ile Tyr Asn Asn Tyr Tyr Asn Asp Ile Gln
 370 375 380
 Asp Thr Gly Ile Asn Ser Arg Met Gly Ala Val Ile Arg Ile Glu Asn
 385 390 395 400
 Asn Val Phe Glu Asn Ala Lys Asn Pro Ile Val Ser Phe Tyr Ser Ser
 405 410 415
 Gly Tyr Gly Tyr Trp Asp Thr Arg Gly Asn Ser Phe Ser Asn Ile Thr
 420 425 430
 Trp Gln Glu Tyr Pro Ser Asp Gly Ile Ile Ala Gly Pro Asn Val Gln
 435 440 445
 Pro Thr Ala Val Leu Asn Leu Pro Tyr Ser Phe Asn Leu Leu Pro Thr
 450 455 460
 Asn Gln Val Lys Ala His Val Leu Ala Asn Ala Gly Val Asn Lys Cys
 465 470 475 480
 Ser Phe

<210> 129
 <211> 1173
 <212> DNA
 <213> *Bacillus halodurans* ATCC 27557

<220>

<400> 129

atgagttcga	aaatcaaaaa	tgctatcaat	aactatagtg	ttattattct	cgatggctcg	60
aatggcgatt	ttacagtcaa	tgctacaatg	agttttagtg	gcaagtccaa	taaaactatt	120
gtgggtgtga	acaatgctcg	cctatgcacc	aaattctaca	ttacgccccg	gataaaagaa	180
gcctcgatg	ctgcccgtgt	gaaatctaag	agctcaagta	gtggcactgg	tggactctt	240
tctaattggta	cgtcgtcag	tgaggctcgc	gaattggcta	ctcgtaaac	gttgattgtat	300
tatctcggcg	atagctcaga	atcgatcag	aaagctggta	tctttggctt	tagcaactgc	360
actaatatta	ttatgcgcaa	cattgtttc	gttggccctg	gtccatgcga	tgttagtggc	420
aacgacttgc	tttcgctcgt	tggcgaag	catttctggg	tcgaccactg	cgagtttacc	480
gatggcatcg	atggcaactt	cgacatcacc	aagagtagcg	acttcaacac	cgttcgtgg	540
tgcactttca	gctataccga	ccgcccatac	gaccacatga	attccaacct	tattggtagc	600
tccgattcag	agaatgcggc	ttacctaatt	actactatgg	cttccaacgt	ctggggcaat	660
aagtgcatac	agcgtatgcc	tatggctcgt	gcccgtataa	ttcacctcgt	aaataattat	720
tacaactgccc	ctggcaatag	cgtggctgtg	aatccctcgca	aaaactcaga	attttggtg	780
gagaattgct	atttcgcaag	tggcgttaag	cctttctcgc	agagcggcgc	tcttagctat	840
ctatttatcg	attgctacac	cgaagataact	tacaccttcc	agaaaatctgg	ctctactacg	900
gtgccataca	catatacgaa	attcgatgct	cagctgttc	ccgagcaact	cacccaattc	960
gctggcgcaa	cattgacttc	gccgcttgg	attggtaggg	aatctgagaa	tgttacacca	1020
gtctcagtca	ttgctgcaaa	tagcgatgtc	atatctgtag	aatactatcc	gctcactggc	1080
aagcgcatac	gcgaaccaac	taaaggcattc	aatatcgta	gaactattta	tactaacggc	1140
aacgtgacca	cacaaaaggt	cttggtaaa	taa			1173

<210> 130

<211> 390

<212> PRT

<213> Bacillus halodurans ATCC 27557

<220>

<221> DOMAIN

<222> (38)...(326)

<223> Catalytic domain

<400> 130

Met	Ser	Ser	Lys	Ile	Lys	Asn	Ala	Ile	Asn	Asn	Tyr	Ser	Val	Ile	Ile
1				5					10						15
Leu	Asp	Gly	Ser	Asn	Gly	Asp	Phe	Thr	Val	Asn	Ala	Thr	Met	Ser	Phe
							20		25						30
Ser	Gly	Lys	Ser	Asn	Lys	Thr	Ile	Val	Gly	Val	Asn	Asn	Ala	Arg	Leu
							35		40						45
Cys	Thr	Lys	Phe	Tyr	Ile	Thr	Pro	Glu	Ile	Lys	Glu	Ala	Leu	Asp	Ala
							50		55						60
Ala	Asp	Val	Lys	Ser	Lys	Ser	Ser	Ser	Gly	Thr	Gly	Gly	Thr	Leu	
							65		70		75				80
Ser	Asn	Gly	Thr	Ser	Val	Ser	Glu	Ala	Arg	Glu	Leu	Ala	Thr	Arg	Gln
							85		90						95
Thr	Leu	Ile	Asp	Tyr	Leu	Gly	Asp	Ser	Ser	Glu	Ser	Tyr	Gln	Lys	Ala
							100		105						110
Gly	Ile	Phe	Gly	Phe	Ser	Asn	Cys	Thr	Asn	Ile	Ile	Met	Arg	Asn	Ile
							115		120						125
Val	Phe	Val	Gly	Pro	Gly	Pro	Cys	Asp	Val	Gly	Gly	Asn	Asp	Leu	Leu
							130		135						140
Ser	Leu	Val	Gly	Ser	Lys	His	Phe	Trp	Val	Asp	His	Cys	Glu	Phe	Thr
							145		150						160
Asp	Gly	Ile	Asp	Gly	Asn	Phe	Asp	Ile	Thr	Lys	Ser	Ser	Asp	Phe	Asn
							165		170						175
Thr	Val	Ser	Trp	Cys	Thr	Phe	Ser	Tyr	Thr	Asp	Arg	Ala	Tyr	Asp	His
							180		185						190
Met	Asn	Ser	Asn	Leu	Ile	Gly	Ser	Ser	Asp	Ser	Glu	Asn	Ala	Ala	Tyr
							195		200						205

Leu Asn Thr Thr Met Ala Ser Asn Val Trp Gly Asn Lys Cys Asn Gln
 210 215 220
 Arg Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Tyr
 225 230 235 240
 Tyr Asn Cys Pro Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser
 245 250 255
 Glu Phe Leu Val Glu Asn Cys Tyr Phe Ala Ser Gly Val Lys Pro Phe
 260 265 270
 Ser Gln Ser Gly Ala Leu Ser Tyr Leu Phe Ile Asp Cys Tyr Thr Glu
 275 280 285
 Asp Thr Tyr Thr Phe Gln Lys Ser Gly Ser Thr Thr Val Pro Tyr Thr
 290 295 300
 Tyr Ser Lys Phe Asp Ala Gln Leu Val Pro Glu Gln Leu Thr Gln Phe
 305 310 315 320
 Ala Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Ser Glu
 325 330 335
 Asn Val Thr Pro Val Ser Val Ile Ala Ala Asn Ser Asp Val Ile Ser
 340 345 350
 Val Glu Tyr Tyr Ser Leu Thr Gly Lys Arg Ile Ser Glu Pro Thr Lys
 355 360 365
 Gly Ile Asn Ile Val Arg Thr Ile Tyr Thr Asn Gly Asn Val Thr Thr
 370 375 380
 Gln Lys Val Leu Val Lys
 385 390

<210> 131

<211> 972

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 131

atggcaaaaa tactgacatt agacggtaac ccggccgcca gctggttcaa	caaatccagg	60
accaagtgga atagcagccg cgccgatatt gtgttgtctt accagcaatc	caacggcggt	120
tggccaaaaa acctggatta caactcagtg agcgcaggca atggcgggag	cgacacgcgc	180
accatcgaca atggtcaac cattaccgaa atggtttacc tcgctgaaat	ttataaaaaac	240
ggcggcaaca ccaaatatcg ccatgcagtg cgccagagcag	caaacttttt	300
caatacagca caggcgccctt gccacaattt tatccgtga aaggcggcta	tgcggatcat	360
gcgaccctta acgataacgg catggcgtac gcgttgacgg tattggattt	cgcagtaaac	420
aaacgcgcac cgtttgataa cgacattttc tctgattctg atcggcgaa	attcaaaaacc	480
gctgttgcca aaggtgtgga ttacattttta aaagcgcagt gaaaaacaaa	tggaaaaactc	540
actgcatggt gtgcacaaca cgtgtctacg gattaccaac	cgaaaaaaagc	600
gatgtttttt gatgtttttt gatgtttttt gatgtttttt	gatgcggatcat	660
ccacaaaccg cgaaatcga agcggcggtc aaggcgggtg tcaactgggt	cgccagtcca	720
aataacttatt tggctaacta cacttacgt tcatcaaaag cgtctaccaa	cccgattgtg	780
tataaatccg gaagcagaat gtggtatcgc ttctatgacc tgaacaccaa	ccgtggtttc	840
tttagtgatc gcgatggcag caaattctat gatattcaccc aaatgtcaga	agagcgtcgc	900
accggttata gctgggttgg ctcttacggt gaatcttata ttcccttcgc	gaaaaaagtg	960
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<210> 132

<211> 323

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 132

Met Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro Ala Ala Ser Trp Phe
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Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg Ala Asp Ile Val Leu
 20 25 30

Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn
 35 40 45

Ser Val Ser Ala Gly Asn Gly Ser Asp Ser Gly Thr Ile Asp Asn
 50 55 60

Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Ile Tyr Lys Asn
 65 70 75 80

Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe
 85 90 95

Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro
 100 105 110

Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn Asp Asn Gly Met
 115 120 125

Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn Lys Arg Ala Pro
 130 135 140

Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala Lys Phe Lys Thr
 145 150 155 160

Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala Gln Trp Lys Gln
 165 170 175

Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly Ala Thr Asp Tyr
 180 185 190

Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Ser
 195 200 205

Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Ala
 210 215 220

Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp Phe Ala Ser Pro
 225 230 235 240

Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr
 245 250 255

Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met Trp Tyr Arg Phe Tyr
 260 265 270

Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys
 275 280 285

Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser
 290 295 300

Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser Phe Ala Gln Lys Val
 305 310 315 320

Gly Tyr Leu

<210> 133

<211> 972

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated polynucleotide

<400> 133

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tggccaaaaa acctggatta caactcagtg agcgcaggca atggcgggag	cgacagcggc	180
accatcgaca atggtgcaac cattaccgaa atggtttacc tcgctgaaat	ttataaaaaac	240
ggcggcaaca ccaaataatcg cgatgcagtg cgcaagagcag	caaactttt agtgagctcg	300

caatacagca caggcgcctt	gccacaattt	tatccgttga	aaggcggcta	tcatgatcat	360
gcgaccttta acgataaacgg	catggcgta	gcgttgcgg	tattggattt	cgcagtaaac	420
aaacgcgcac cgttgataa	cgacattttc	tctgattctg	atcgggcgaa	attcaaaacc	480
gctgttgcca aaggtgtgga	ttacattttta	aaagcgcagt	gaaaaacaaa	tggaaaactc	540
actgcattgt gtgcacaaca	cggtgccttg	gattaccaac	cgaaaaaagg	tcgcgttat	600
gaatttggaaat cattgagtgg	taaggagtgc	gtcggcattc	tcgccttctt	gatgacccaa	660
ccacaaaaccg cgaaatcga	agcggcggtc	aaggcgggtg	tcaactgggtt	cgccagtcca	720
aatacttatt tggctaacta	cacttacgat	tcataaaaag	cgtctaccaa	cccgattgtg	780
tataaaaagg gaagcagaat	gtggtatcgc	ttctatgacc	tgtataccaa	ccgtggttc	840
tttagtgate gcatggcag	caaattctat	gatatcaccc	aatgtcaga	agagcgtcgc	900
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<210> 134

<211> 323

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated polypeptide

<400> 134

Met	Ala	Lys	Ile	Leu	Thr	Leu	Asp	Gly	Asn	Pro	Ala	Ala	Ser	Trp	Phe		
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Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Ser	Ser	Arg	Ala	Asp	Ile	Val	Leu		
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Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys	Asn	Leu	Asp	Tyr	Asn		
														35	40	45	
Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Asp	Ser	Gly	Thr	Ile	Asp	Asn		
														50	55	60	
Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu	Ala	Glu	Ile	Tyr	Lys	Asn		
														65	70	75	80
Gly	Gly	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val	Arg	Arg	Ala	Ala	Asn	Phe		
														85	90	95	
Leu	Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala	Leu	Pro	Gln	Phe	Tyr	Pro		
														100	105	110	
Leu	Lys	Gly	Gly	Tyr	His	Asp	His	Ala	Thr	Phe	Asn	Asp	Asn	Gly	Met		
														115	120	125	
Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val	Asn	Lys	Arg	Ala	Pro		
														130	135	140	
Phe	Asp	Asn	Asp	Ile	Phe	Ser	Asp	Ser	Asp	Arg	Ala	Lys	Phe	Lys	Thr		
														145	150	155	160
Ala	Val	Ala	Lys	Gly	Val	Asp	Tyr	Ile	Leu	Lys	Ala	Gln	Trp	Lys	Gln		
														165	170	175	
Asn	Gly	Lys	Leu	Thr	Ala	Trp	Cys	Ala	Gln	His	Gly	Ala	Leu	Asp	Tyr		
														180	185	190	
Gln	Pro	Lys	Lys	Gly	Arg	Ala	Tyr	Glu	Leu	Glu	Ser	Leu	Ser	Gly	Lys		
														195	200	205	
Glu	Ser	Val	Gly	Ile	Leu	Ala	Phe	Leu	Met	Thr	Gln	Pro	Gln	Thr	Ala		
														210	215	220	
Gln	Ile	Glu	Ala	Ala	Val	Lys	Ala	Gly	Val	Asn	Trp	Phe	Ala	Ser	Pro		
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Asn	Thr	Tyr	Leu	Ala	Asn	Tyr	Thr	Tyr	Asp	Ser	Ser	Lys	Ala	Ser	Thr		
														245	250	255	
Asn	Pro	Ile	Val	Tyr	Lys	Lys	Gly	Ser	Arg	Met	Trp	Tyr	Arg	Phe	Tyr		
														260	265	270	
Asp	Leu	Tyr	Thr	Asn	Arg	Gly	Phe	Phe	Ser	Asp	Arg	Asp	Gly	Ser	Lys		
														275	280	285	
Phe	Tyr	Asp	Ile	Thr	Gln	Met	Ser	Glu	Glu	Arg	Arg	Thr	Gly	Tyr	Ser		

290 295 300
Trp Gly Gly Ser Trp Gly Glu Val Ile Ile Ser Phe Ala Gln Lys Val
305 310 315 320
Gly Tyr Leu